

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 13:08:48 ; Search time 57.7 Seconds
(without alignments)
311.854 Million cell updates/sec

Title: US-09-747-155-225

Perfect score: 825
Sequence: 1 VAICNPPLVPMWMSNKLIAO.....LAEDQKVSFLYTIIPLL 162

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	825	100.0	162	22	AAG98518
2	825	100.0	162	22	AAAG72109
3	825	100.0	162	22	AAAG72421
4	806	97.7	162	22	AAAG98500
5	630	76.4	329	22	AAAG71992
6	547	66.3	319	22	AAAG71531
7	546	66.2	314	22	AAU24633
8	546	66.2	314	22	AAAG71500
9	546	66.2	314	22	AAAG72474
10	527	63.9	162	22	AAAG98487
11	495	60.0	324	22	AAAG71529

12	494	59.9	309	22	AAAG71525	Human olfactory re
13	494	59.9	325	22	AAU24632	Human olfactory re
14	477.5	57.9	310	22	AAAG71502	Human olfactory re
15	471	57.1	314	22	AAAG71522	Human olfactory re
16	440	53.3	314	22	AAAG71945	Human olfactory re
17	436	52.8	315	22	AAAG71520	Human olfactory re
18	416	50.4	311	22	AAAG71532	Human olfactory re
19	416	50.4	316	22	AAU24535	Human olfactory re
20	414	50.2	312	22	AAAG73043	Human olfactory re
21	411	49.8	314	22	AAAB20487	Human G protein co
22	408	49.5	312	22	AAAG73045	Olfactory receptor
23	407	49.3	312	22	AAAG73044	Olfactory receptor
24	407	49.3	314	22	AAAB20486	Human G protein co
25	406	49.2	320	22	AAAG71832	Murine OR-like pol
26	401.5	48.7	333	22	AAAG72682	Murine OR-like pol
27	400	48.5	301	22	AAAG66341	Partial NOV 2 prot
28	400	48.5	312	22	AAAG71610	Human olfactory re
29	400	48.5	312	22	AAAG72568	Human OR-like pol
30	400	48.5	312	22	AAAG73038	Olfactory receptor
31	400	48.5	314	22	AAU24552	Human olfactory re
32	400	48.5	314	22	AAAG66322	Human NOV 2 protei
33	400	48.5	328	22	AAAG71644	Human olfactory re
34	400	48.5	343	22	AAAG72665	Murine OR-like pol
35	400	48.5	314	22	AAU24579	Human olfactory re
36	398	48.2	314	22	AAU24763	Human olfactory re
37	396	48.0	316	22	AAU24697	Human olfactory re
38	396	48.0	324	22	AAU24697	Human olfactory re
39	384	47.8	318	22	AAAG73040	Olfactory receptor
40	383	47.6	317	22	AAU24664	Human olfactory re
41	393	47.6	317	22	AAAG71834	Human olfactory re
42	392	47.5	310	22	AAAG71819	Human olfactory re
43	391	47.4	313	22	AAAG71718	Human olfactory re
44	391	47.4	318	22	AAAG73042	Olfactory receptor
45	389	47.2	292	21	AAV90875	Human G protein co

ALIGNMENTS

RESULT 1	AAAG98518	standard; Protein; 162 AA.
XX	AAAG98518;	
AC	25-SEP-2001 (first entry)	
XX		
DE	Human olfactory receptor 1.	
XX		
KW	Olfactory receptor; primate; mouse; human; food processing industry;	
KM	aromas; perfumery; toxic substance.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200146262-A2.	
XX		
PD	28-JUN-2001.	
XX		
PF	22-DEC-2000; 2000WO-1B02017.	
XX		
PR	22-DEC-1999; 99US-0171746.	
PR	21-DEC-2000; 2000US-0747155.	
XX		
PA	(CNRS) CNRS CENT NAT RECH SCI.	
PI	Rouquier S, Giorgi D;	
XX		
DR	WPI: 2001-381911/40.	
XX	N-PsDB; AAH84009.	
XX		
PT	Nucleic acids encoding primate and murine olfactory receptors, useful	
XX	for analysis odours e.g. in food processing and perfumery -	

PS Claim 3; page 266; 482pp; English.

XX The invention relates to olfactory receptors (AAG398432-AAG398609) and the
CC genes encoding them (AAH33879-AAH4411) including pseudogenes of 10
CC prime species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis). In perfumery (e.g. for the analysts
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours).

SQ **Sequence** **162 AA;**

Query Match	100.0%	Score 825;	DB 22;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 2,8e+93;		
Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 VAICNPLLYPYMMSNKLSSAQLLSISYIGFLPLVHVSLLRLTEFCRNIHHFYCEILQ 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 valcnp1llypymmsnklssaqlslsyyigflplvvhssllrltfcrcfnllhyceelq 60

QY 61 LKTSICNGPSTINALIFIFGAFIPIPLMTIIISYTRVLPDILKKSEKSKAFSTCGA 120
|||||
61 LKTSICNGPSTINALIFIFGAFIPIPLMTIIISYTRVLPDILKKSEKSKAFSTCGA 120
|||||

Qy 121 HLSSVSLYGTFLFMVYRPAAGLAEDDQKYSLEFYTIIPIL 162
|||||
Db 121 hllsvsllygtflfmvyrpasglaedqkyslytllipil 162

RESULT 2
AAG72109
ID: 11072100 standard. Protocols: 153 M

XX
XX
AC AAG72109;
ID AAG72109 standard; PLOEHL; 102 AA.
XX
XX 30-TM-2001 /first contrl

Human olfactory receptor polypeptide, SEQ ID NO: 1790.

XX secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.

XX homo sapiens.
XX
PN W0200127158-A2.
XX
18-APR-2001
PD

FD 13 SEP 2001.
XX
XX
PF 06-OCT-2000; 2000MO-US27582.
XX
XX 08-OCT-1999; 00US-0158615
XX

PA (DIGI -) DIGISCENTS.
PA (VEDA) VEDA RES & DEV CO LTD
XX 24-FEB-2000; 2000US-0184809.
PR 00 003 12221 2000 0180003.
PA 00 003 12221 2000 0180003.

XX
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPT: 2001-290713/30
DR

XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX

PS Claim 11, page 1178; 1657pp; English.

combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals.

Sequence 162 AA;

Query Match	100.0%	Score 825;	DB 22;	Length 162;
Best Local Similarity	100.0%	Pred. No. 2.8e-93;		
Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 VAICNPILLYPYVMNSNKLQAQLLSIVYIGFLPHLVHVSLLRLTFCRENIITHYPECIIQ 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 1 vaicnpilypvmnsnklasaqlslstsyigflphlvhsllrltfcrcfnlhyecellq 60

QY 61 LFKISCNCEPINALIIFEGAFIQIPMTITISYTRVLFPIEKKSEKSKAFSCGCA 120
|||||
61 lfkiscngpsinaliiffegafiqipmtitisytrvlfllkkseksgskafscgca 120

QY 121 HLLSVLYGFLIFMYVRPASGLAEDDKVYSLEFYTIIPLL 162
|||||
Db 121 hllsvlygflifmyvrpasglaeddkvyslyftiiprl 162

RESULT	3
AA672421	
1D 1A672421	standard. Protein. 162 AA

1D MAG/2421 Standard, F100nm, 100 nm.
 1X
 2X
 AC MAG/2421;
 XX
 30-THU -2001 (first entry)
 cm

Human: olfactory receptor. OR, primary scent determination;
 Human: OR-like polypeptide query sequence, SEQ ID NO: 2102.
 Human: OR-200A (first entry)
 XX
 XX
 DE
 XX

XX Homo sapiens
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation.
 SS

xx memo Dependent
xx
PN W0200127158-A2.
xx
19-APR-2001
DN

XX 06-OCt-2000; 2000WO-US27582.
XX 08-OCt-1999; 99US-0158615.
XX

EN 00 DEC 2000 0000
 PR 24-FEB-2000; 2000US-0184809.
 XX
 (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA

XX
XX
PI Bellenson J, Smith D, Lancel D, Glusman G, Fuchs T, Yanai I;
XX
XX
DR WPI: 2001-290713/30.

XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
PT

Example 6, Page 1411-1412; 1857pp; English.

CC and the identification of combinations of odour receptors that are
CC involved in detecting such secondary scents. This enables the
CC construction of a scent representation (also called a scent fingerprint
CC or scent profile), which may be used to re-create and edit scents.
CC Libraries of olfactory receptors are useful for determining the
CC interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals.

SO Sequence 162 AA;

Query Match 100.0%; Score 825; DB 22; Length 162;
Best Local Similarity 100.0%; Pred. No. 2.8e-93;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPILPYVMNSKLSAQSLISYVIGFLHPLVHSLRLTRCERNIHFFCEIIQ 60
DB 1 vaicnpilpyvmnsnklsaqslisyvigflhplvhsllrltrcernihffceiiq 60

OY 61 LFKISGNSPINALIIFIFGAFIQIPLMTIIISYTRVLFDLKKKSEKGRKAPSTCGA 120
DB 61 lfkisgnspsinaliififgafiqiplmtiisylrvlfdllkkksekgrskatscga 120

OY 121 HLLSVSLYGYTLIFMYVRPASGLAEDODKVSLSFTYIIIPPL 162
DB 121 hllsvsllygltifmyvrpasglaedodkvslyftiilppl 162

RESULT 4

AAG98500
ID AAG98500 standard; Protein; 162 AA.

AC AAG98500;

DT 25-SEP-2001 (first entry)

DE Pan troglodytes olfactory receptor 9.

KM Olfactory receptor; primate; mouse; human; food processing industry;

KW aromas; perfumery; toxic substance.

OS Pan troglodytes.

PN WO200146262-A2.

PD 28-JUN-2001.

PF 22-DEC-2000; 2000WO-1B02017.

PR 22-DEC-1999; 99US-0171746.

PR 21-DEC-2000; 2000US-0747155.

PA (CNRS) CNRS CENT NAT RECH SCI.

PI Rouquier S, Giorgi D;

DR WPI: 2001-381911/40.

DR N-PSDB; AAH83985.

PT Nucleic acids encoding primate and murine olfactory receptors, useful
for analysis odours e.g. in food processing and perfumery -

PS Claim 3; Page 226; 482pp; English.

CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours).

SO Sequence 162 AA;

Query Match 97.7%; Score 806; DB 22; Length 162;
Best Local Similarity 97.5%; Pred. No. 6e-91;
Matches 158; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VAICNPILPYVMNSKLSAQSLISYVIGFLHPLVHSLRLTRCERNIHFFCEIIQ 60
DB 1 vaicnpilpyvmnsnklsaqslisyvigflhplvhsllrltrcernihffceiiq 60

OY 61 LFKISGNSPINALIIFIFGAFIQIPLMTIIISYTRVLFDLKKKSEKGRKAPSTCGA 120
DB 61 lfkisgnspsinaliififgafiqiplmtiisylrvlfdllkkksekgrskatscga 120

OY 121 HLLSVSLYGYTLIFMYVRPASGLAEDODKVSLSFTYIIIPPL 162
DB 121 hllsvsllygltifmyvrpasglaedodkvslyftiilppl 162

RESULT 5

AAG71992
ID AAG71992 standard; Protein; 329 AA.

AC AAG71992;

DT 31-JUL-2001 (first entry)

DE Human olfactory receptor polypeptide, SEQ ID NO: 1673.

KM Human; olfactory receptor; OR; primary scent determination;

KW secondary scent determination; polypeptide library; odour receptor;

KW scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

PN WO200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI: 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory
sensations for identifying olfactory agonists and antagonists -

PS Claim 11; Page 1092-1093; 1857pp; English.

CC The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals.

SO Sequence 329 AA;

Seq	Sequence	314	AA;
Qy	Query Match	66.2%;	Score 546; DB 22; Length 314;
Best	Local Similarity	64.8%;	Fred. No. 1.3e-58;
Matches	105; Conservative	23;	Mismatches 34; Indels 0; Gaps 0;
Qy	1	VAICNPDLIPVWMSNKL	SAQLLSISVYIGTGLPLVHLSLLTEPCRENIHYFYCELIQ 60
Db	129	vaicpdllypvmmsncrlrlafsfllgflhalthevllfflfcnsllhhfyodlilp 188	
Qy	61	LEKISNGSIALILFIIFGAFIOIPLMTLTIISYTRVYFDLKKRSEKGRKASTGCA 120	
Db	189	lfmisdcpnsflnmvflfslgslyftlvtvlnsyftalfllkkksvgyvkatstoga 248	
Qy	121	HLISLYYGTILFIEMVVRPASGLAEDODKYSLEFTTIIPPL 162	
Db	249	hlisvsiyygplilfmylfpaspqaddqmdsfvyltllppl 290	

	Query Match	Score 546;	DB 22;	Length 314;
	Best Local Similarity	64.8%;	Pred. No. 1,3e-58;	
	Matches 105;	Conservative 23;	Mismatches 34;	Indels 0; Gaps 0.
QY	1 VAICNPDLIYPVMMSKLSQAOLISIVSIGTFLPLVHVSLLRLTECFRNIIMHYFCETIQ	60		
	: : : : : : : : : : : : : : : :			
Db	129 vaickplpyvimnslcirrlafsfglfhalheviilffctfcensllnhfyccidip	188		
QY	61 LFKICNGPSINALIIFFGAFGIPTLMTIIISTRVILFDLKKSSEGRKASTGCA	120		
	: : : : : : : : : : : : : : : :			
Db	189 lfmiscotpslnflmwflilsgsiqvlvtvlnsvyfaflfklikksrvgrvkastcga	248		
QY	121 HLISLVLYGTLLFPMYVRPASGLADODKVSLFPTIIIRPL	162		
	: : : : : : : : : : : : : : : :			
Db	249 hlisvlygprlfnmylrpasppaddqdmdsvfyllipll	290		

RESULT	8
ID	AAG71500
XX	AAG71500 standard; Protein; 314 AA.
AC	
XX	
XX	AAG71500;
DT	30-JUL-2001 (first entry)
XX	
DE	Human olfactory receptor polypeptide, SEQ ID NO: 1181.
XX	
KW	Human: olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
XX	
OS	Homo sapiens.
PN	WO2001271158-A2.
XX	
PD	19-APR-2001.
XX	
PF	06-OCT-2000; 2000MO-US27582.
XX	
PR	08-OCT-1999; 99US-0158615. 24-FEB-2000; 2000US-0184809.
PA	(DIGI-) DIGISCENTS.
PA	(YEDA) YEDA RES & DEV CO LTD.
PI	Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
DR	WPI; 2001-290713/30.
PT	New polynucleotides which encode polypeptides involved in olfactory sensitation for identifying olfactory agonists and antagonists -
PS	Claim 11; Page 697-698; 1857pp; English.
CC	The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals.
Sequence	314 AA:

XX	RESULT	9
XX	AAG72474	
ID	AAG72474	standard; Protein: 314 AA.
XX		
AC	AAG72474;	
XX		
DT	30-JUL-2001	(first entry)
XX		
DE	Human OR-1-like polypeptide query sequence, SRO ID NO: 2155.	
XX		
KW	Human; olfactory receptor; OR; primary scent determination;	
KW	secondary scent determination; polypeptide library; odour receptor;	
KW	scent profile; scent fingerprint; scent representation.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200127158-A2.	
XX		
PD	19-APR-2001.	
XX		
PF	06-OCT-2000; 2000WO-US27582.	
XX		
PR	08-OCT-1999; 99US-0158615.	
PR	24-FEB-2000; 2000US-0184809.	
XX		
PA	(DIGI-) DIGISCENTS.	
PA	(YEDA) YEDA RES & DEV CO LTD.	
XX		
PI	Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;	
DR	WPI; 2001-290713/30.	
XX		
PT	New polynucleotides which encode polypeptides involved in olfactory	
PT	sensation for identifying olfactory agonists and antagonists -	
XX		
PS	Example 6; Page 1448-1449; 1857pp; English.	
XX		
XX	The present sequence is a polypeptide encoded by one of 344 newly mined	
XX	human genes. It was used as a query sequence in a database search of	
CC	olfactory receptor (OR)-like sequences. The invention relates to isolated	
CC	polynucleotides encoding polypeptides involved in olfactory sensation.	
CC	The polynucleotides can be used in screening for olfactory agonists and	
CC	antagonists. The methods allow for the determination of primary scents	
CC	and the identification of the odour receptors used to detect these	
CC	primary scents. The methods also enable determination of secondary scents	
CC	and the identification of combinations of odour receptors that are	
CC	involved in detecting such secondary scents. This enables the	
CC	construction of a scent representation (also called a scent fingerprint	
CC	or scent profile), which may be used to re-create and edit scents.	
CC	Libraries of olfactory receptors are useful for determining the	
CC	interaction pattern of a composition with the receptors, and can be	
CC	used for determining differences in the olfactory faculties of different	
XX	individuals.	
XX		
SQ	Sequence	314 AA;

Query Match 66.2%; Score 546; DB 22; Length 314;
 Best Local Similarity 64.8%; Pred. No. 1.3e-58;
 Matches 105; Conservative 23; Mismatches 34; Indels 0; Gaps 0;

OY 1 VAICNPILYPMWMSNKLQAOLLSIVYIGFLPHVHSLRLRFECPNIIHYECETIQ 60
 ||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 DB 129 valckpillypvmmsncslrlaatsfllgflhalhevlfrlfcnsnlhhydcldlp 188

OY 61 LFKISGNPSINALIIFFGAFIOIPTLMTIIISYTRVLDILKKKSEKGRKAFSTCGA 120
 ||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 DB 189 lfmsccdpnsinfilmslqfvtlvynsftalfllkkksvgyvrkaftscga 248

OY 121 HLISVSLYGTILFMYVRPASGLAEDODKYSLFTYIIIPLL 162
 ||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 DB 249 hllsvsllygpllfmylrpsapqddqmdsvfvtllp 290

RESULT 10
 AAG98487 standard; Protein: 162 AA.
 XX
 AC AAG98487;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Papilio hamadryas olfactory receptor 12.
 XX
 KM olfactory receptor; primate; mouse; human; food processing industry;
 KM aromas; perfumery; toxic substance.
 XX
 OS Papilio hamadryas.
 XX
 PN WO200146262-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 22-DEC-2000; 2000WO-1B02017.
 XX
 PR 22-DEC-1999; 99US-0171746.
 PR 21-DEC-2000; 2000US-0747155.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Rouquier S, Giorgi D;
 XX
 DR WPI: 2001-381911/40.
 DR N-PSDB; AAH83971.
 XX
 PT Nucleic acids encoding primate and murine olfactory receptors, useful
 XX for analysis odours e.g. in food processing and perfumery -
 XX
 PS Claim 3; Page 199; 482pp; English.
 XX
 CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
 CC genes encoding them (AAH8379-AAH8431) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours).
 CC
 XX
 SQ Sequence 162 AA;

Query Match 63.9%; Score 527; DB 22; Length 162;
 Best Local Similarity 62.3%; Pred. No. 1.2e-56;
 Matches 101; Conservative 22; Mismatches 39; Indels 0; Gaps 0;

OY 1 VAICNPILYPMWMSNKLQAOLLSIVYIGFLPHVHSLRLRFECPNIIHYECETIQ 60
 ||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 DB 1 valckpillypvmmsncslrlaatsfllgflhalhevlfrlfcnsnlhhydcldlp 60

OY 61 LFKISGNPSINALIIFFGAFIOIPTLMTIIISYTRVLDILKKKSEKGRKAFSTCGA 120
 ||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 DB 61 lltscdpnsinfilmslqfvtlvynsftalfllkkksvgyvrkaftscga 120

OY 121 HLISVSLYGTILFMYVRPASGLAEDODKYSLFTYIIIPLL 162
 ||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 DB 121 hllsvsllygpllfmylrpsapqddqmdsvfvtllp 162

RESULT 11
 AAG71529
 ID AAG71529 standard; Protein: 324 AA.
 XX
 AC AAG71529;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1210.
 XX
 KM Human; olfactory receptor; OR; primary scent determination;
 KM secondary scent determination; polypeptide library; odour receptor;
 KM scent profile; scent fingerprint; scent representation.
 XX
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US27582.
 XX
 PR 08-OCT-1999; 99US-0158615.
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX
 DR WPI: 2001-290713/30.
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 PS Claim 11; Page 720-721; 1857pp; English.
 XX
 CC The present sequence is an olfactory receptor which is encoded by
 CC one of a number of novel polynucleotides. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification
 CC of the odour receptors used to detect these primary scents. The methods
 CC also enable determination of secondary scents and the identification of
 CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC faculties of different individuals.
 CC
 XX
 SQ Sequence 324 AA;

Query Match 60.0%; Score 495; DB 22; Length 324;
 Best Local Similarity 61.7%; Pred. No. 2.5e-52;
 Matches 100; Conservative 19; Mismatches 43; Indels 0; Gaps 0;

OY 1 VAICNPILYPMWMSNKLQAOLLSIVYIGFLPHVHSLRLRFECPNIIHYECETIQ 60
 ||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 DB 124 valckpillypvmmsncslrlaatsfllgflhalhevlfrlfcnsnlhhydcldlp 183

OY 61 LFKISGNPSINALIIFFGAFIOIPTLMTIIISYTRVLDILKKKSEKGRKAFSTCGA 120

Db 184 lllkscstsflnflmvlfnadsiqvfllgtlllsytlvlllllhkksvvgikavstcga 243
OY 121 HLLSVSLYYGTLIFMWVRPASPGLAEDODKVSLEFYTIIIPLL 162
Db 244 hllsvsllygpltfkylgsaspqaddqdmesslftvlp1l 285

RESULT 12

AA671525
ID AAG71525 standard; Protein; 309 AA.

AC AAG71525;

DT 30-JUN-2001 (first entry)

DE Human olfactory receptor polypeptide, SEQ ID NO: 1206.

KW Human; olfactory receptor; OR: primary scent determination;

KM secondary scent determination; polypeptide library; odour receptor;

OS scent profile; scent fingerprint; scent representation.

XX Homo sapiens.

PN WO200127158-A2.

PD 19-APR-2001.

PE 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

PA (DIGIT-) DIGISCENTS.

PI (YEDA) YEDA RES & DEV CO LTD.

XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX WPI: 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory

XX sensation for identifying olfactory agonists and antagonists -

PS Claim 11; Page 717 and 684; 1857pp; English.

XX The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC facilities of different individuals.

XX Sequence 309 AA;

XX Query Match 59.9%; Score 494; DB 22; Length 309;

XX Best Local Similarity 59.9%; Pred. No. 3.1e-52;

XX Matches 97; Conservative 24; Mismatches 41; Indels 0; Gaps 0;

OY 1 VAICNPILYPVMSNKLISQSLISYVIGFLPVLVHVSLLRTFCRFNIHYFCEIIQ 60
Db 124 vaicallpvlmtncelcqlvlvstfgllhllhaeatsfrltfonsnllqbfydcilp 183
OY 61 LEKISCNPSINALIFIFGAFIQIPTLMTIISYTRVLEFDILKKSEGRSKAFSTCGA 120
Db 184 lllkscstsflnflmvlfnadsiqvfllgtlllsytlvlllllhkksvvgikavstcga 243

OY 121 HLLSVSLYYGTLIFMWVRPASPGLAEDODKVSLEFYTIIIPLL 162
Db 244 hllsvsllygpltfkylgsaspqaddqdmesslftvlp1l 285

RESULT 13

AAU24632
ID AAU24632 standard; Protein; 325 AA.

AC AAU24632;

DT 18-DEC-2001 (first entry)

DE Human olfactory receptor AOLFRI26.

KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;

KM food additive; cosmetic; fragrance; pharmaceutical additive.

OS Homo sapiens.

PN WO200168805-A2.

PD 20-SEP-2001.

PE 13-MAR-2001; 2001WO-US07771.

PR 13-MAR-2000; 2000US-0188914.

PR 24-MAR-2000; 2000US-0192033.

PR 12-APR-2000; 2000US-0198474.

PR 24-APR-2000; 2000US-0199335.

PR 26-MAY-2000; 2000US-0207702.

PR 23-JUN-2000; 2000US-0213849.

PR 16-AUG-2000; 2000US-0226534.

PR 07-SEP-2000; 2000US-0230732.

PR 07-FEB-2001; 2001US-0266862.

XX (SENO-) SENOMYX INC.

XX Zozulya S;

XX WPI: 2001-570867/64.

XX N-PSDB; AAS42325.

PT Nucleic acids encoding human olfactory G protein-coupled receptors,

XX useful for screening for compounds involved in olfactory sensation,

XX where the compounds can be used in the food, pharmaceutical and

XX cosmetic industries to customise odours -

PS Claim 60; Page 136; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory

XX receptors, OR, (a G protein-coupled receptor, GPCR). The OR's

XX specifically recognise molecules, odourants, that elicit specific

XX olfactory sensation. The human olfactory receptors and polynucleotides

XX encoding them are useful for screening a library of chemical compounds

XX for compounds that are involved in olfactory sensation. Modulators of

XX their activity are useful for pharmacological and genetic modulation of

XX olfactory signalling pathways. Therefore, they can be used in the food,

XX pharmaceutical and cosmetic industries to customise odours and

XX fragrances. The present sequence is a human olfactory receptor of the

XX invention.

XX Sequence 325 AA;

XX Query Match 59.9%; Score 494; DB 22; Length 325;

XX Best Local Similarity 59.9%; Pred. No. 3.3e-52;

XX Matches 97; Conservative 24; Mismatches 41; Indels 0; Gaps 0;

OY 1 VAICNPILYPVMSNKLISQSLISYVIGFLPVLVHVSLLRTFCRFNIHYFCEIIQ 60
Db 140 vaicallpvlmtncelcqlvlvstfgllhllhaeatsfrltfonsnllqbfydcilp 199

```

OY 61 LFKISCNPSINALIIFFGAFIOPTLMTIIISYTRVLPDLKKSEKSKAFSTCGA 120
    ||||| ||| :||| ||: | :||| ||| ||||| ||| ||||| |||
DB 200 lfkiscdssinflmvlffscsiqvtlgtlsllytlvlfllkkskvgkrlkafstcga 259
    ||||| ||| :||| ||: | :||| ||| ||||| ||| ||||| |||
OY 121 HLTSVLYGTLFMYVRPASGLAEDODKYSLFETIIIPLL 162
    ||||| ||| :||| ||: | :||| ||| ||||| ||| ||||| |||
DB 260 hltsvlygptlftkylgsaspqaddqdmesllyftvlp11 301
    ||||| ||| :||| ||: | :||| ||| ||||| ||| ||||| |||

RESULT 14
AAG71502
ID AAG71502 standard; Protein: 310 AA.
AC AAG71502;
DT 31-JUL-2001 (first entry)
DE Human olfactory receptor polypeptide, SEQ ID NO: 1183.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
PN MO200127158-A2.
PD 19-APR-2001.
PF 06-OCT-2000; 2000WO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA ) YEDA RES & DEV CO LTD.
PI Bellenson J, Smth D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI: 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
PS Claim 11; Page 698-699; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals.
XX
SQ Sequence 310 AA:

Query Match 57.9%; Score 477.5; DB 22; Length 310;
Best Local Similarity 59.3%; Pred. No. 3.4e-50;
Matches 96; Conservative 21; Mismatches 40; Indels 5; Gaps 1;

OY 1 VALCNPLLYPYMWSKKSLSAQLSTSYVIGLHPVLSLLRLFCRPNIIHYFYCEIQ 60
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||
DB 124 valcnpillypymwtnglctirllg-----glhalihgffrlftcnsnvvhlycdilp 178
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||
OY 61 LFKISCNPSINALIIFFGAFIOPTLMTIIISYTRVLPDLKKSEKSKAFSTCGA 120

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DB 179 lfkiscdssinflmvlffscsiqvtlgtlsllytlvlfllkkskvgkrlkafstcga 238
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||
OY 121 HLTSVLYGTLFMYVRPASGLAEDODKYSLFETIIIPLL 162
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||
DB 239 hltsvlyhgpddfnmgsaspqaddqdmesllyftvlp11 280
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||

RESULT 15
AAG71522
ID AAG71522 standard; Protein: 314 AA.
AC AAG71522;
DT 31-JUL-2001 (first entry)
DE Human olfactory receptor polypeptide, SEQ ID NO: 1203.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
PN MO200127158-A2.
PD 19-APR-2001.
PF 06-OCT-2000; 2000WO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA ) YEDA RES & DEV CO LTD.
PI Bellenson J, Smth D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI: 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
PS Claim 11; Page 715-716; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals.
XX
SQ Sequence 314 AA:

Query Match 57.1%; Score 471; DB 22; Length 314;
Best Local Similarity 58.0%; Pred. No. 2.2e-49;
Matches 94; Conservative 22; Mismatches 46; Indels 0; Gaps 0;

OY 1 VALCNPLLYPYMWSKKSLSAQLSTSYVIGLHPVLSLLRLFCRPNIIHYFYCEIQ 60
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||
DB 123 valcnpillypymwtnglctwllslfsgllhalihgfsyrlftcnsnctihxtcdilp 182
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||
OY 61 LFKISCNPSINALIIFFGAFIOPTLMTIIISYTRVLPDLKKSEKSKAFSTCGA 120
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||
DB 183 lfkiscdssinflmvlffscsiqvtlgtlsllytlvlfllkkskvgkrlkafstcga 242
    ||||| ||||| :||| ||: | :||| ||| ||||| ||| ||||| |||

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OY 121 HLISVSLYYGTLIFMYVRPAPSGIAEDQDKVYSLFYTIIPLL 162
|:| ||||| | ||| | | :||| : ||||:|:|
DB 243 hllpvslyyqplafmygsasqraddqdmneslfytlvlp|| 284

Search completed: June 27, 2002, 14:02:57
Job time: 3249 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2002, 13:08:53 : Search time 24.46 Seconds
(without alignments)
161.772 Million cell updates/sec

Title: US-09-747-155-225

Perfect score: 825

Sequence: 1 VAICNPPLYVWMSNKLQA.....LAEDQKVSLEFTHIPL 162

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents: AA.*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	334	40.5	314	3	US-08-988-876-7
2	318	38.5	284	1	US-08-118-270-67
3	318	38.5	284	5	PCR-US93-08528-67
4	312.5	37.9	296	2	US-08-467-948A-2
5	312.5	37.9	296	3	US-08-467-947A-2
6	311	37.7	222	2	US-08-467-948A-27
7	311	37.7	222	3	US-08-467-947A-27
8	308.5	37.4	277	1	US-08-118-270-68
9	308.5	37.4	277	5	PCR-US93-08528-68
10	304	36.8	316	2	US-08-827-291A-2
11	293	35.5	247	1	US-08-465-980-3
12	293	35.5	247	2	US-09-053-303-3
13	293	35.5	247	5	PCR-US93-07093-3
14	291	35.3	274	1	US-08-118-270-69
15	291	35.3	274	5	PCR-US93-08528-69
16	279	33.8	321	4	US-08-748-506-10
17	279	33.8	321	4	US-08-748-506-18
18	277	33.6	321	4	US-08-748-506-19
19	276	33.5	309	3	US-08-988-876-5
20	276	33.5	321	4	US-08-748-506-11
21	273	33.1	321	4	US-08-748-506-13
22	272	33.0	286	1	US-08-118-270-65
23	272	33.0	286	5	PCR-US93-08528-65
24	269	32.6	284	1	US-08-118-270-61
25	269	32.6	284	5	PCR-US93-08528-61
26	267	32.4	321	4	US-08-748-506-12
27	267	32.4	321	4	US-08-748-506-20

28	267	32.4	327	4	US-08-748-506-22	Sequence 22, Appl
29	267	32.4	327	4	US-08-748-506-23	Sequence 23, Appl
30	263	31.9	327	4	US-08-748-506-24	Sequence 24, Appl
31	259	31.4	333	3	US-08-988-876-6	Sequence 6, Appl
32	252	30.5	327	4	US-08-748-506-14	Sequence 14, Appl
33	250	30.3	275	1	US-08-118-270-66	Sequence 66, Appl
34	250	30.3	275	5	PCR-US93-08528-66	Sequence 66, Appl
35	237	28.7	269	5	US-08-118-270-64	Sequence 64, Appl
36	237	28.7	269	5	PCR-US93-08528-64	Sequence 64, Appl
37	231	28.0	273	1	US-08-118-270-63	Sequence 63, Appl
38	231	28.0	273	5	PCR-US93-08528-63	Sequence 63, Appl
39	228.5	27.7	277	1	US-08-118-270-62	Sequence 62, Appl
40	228.5	27.7	277	5	PCR-US93-08528-62	Sequence 62, Appl
41	219	26.5	293	1	US-08-118-270-60	Sequence 60, Appl
42	219	26.5	293	5	PCR-US93-08528-60	Sequence 60, Appl
43	171	20.7	177	4	US-08-748-506-21	Sequence 21, Appl
44	169	20.5	320	1	US-08-465-980-2	Sequence 2, Appl
45	169	20.5	320	2	US-09-053-303-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-08-988-876-7

Sequence 7, Application US/08988876

Patent No. 6063596

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED

TITLE OF INVENTION: WITH IMMUNE RESPONSE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988,876

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0441 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 314 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 32086

US-08-988-876-7

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-27

Query Match 37.7%; Score 311; DB 2; Length 222;
Best Local Similarity 38.9%; Pred. No. 2.6e-27;
Matches 61; Conservative 36; Mismatches 60; Indels 0; Gaps 0;

QY 1 VAICNPPLYPMVMSNKLQAQLLSISYVIGFLPLVHVSLLRLTFCRPNIIHYFCETIQ 60
DB 64 VAICHPRLYSALMSRVCSTMAVTSMIIIGVLSLHLVLLPLPFCVSKVNHFFCEITA 123
QY 61 LKTSICNGPSINALIIFIFGAFIOIPLMTIISYTRYVLEDILKKSEKRSKAFSTCGA 120
DB 124 ILKLACADTHLENMTVLGAVSVLGPFSSTIVSYACILGAILKIOSHEGOKRAKAFSTCSS 183
QY 121 HLTSVSLYGTILFMVYRPPASGLAEDODKYSLPFTI 157
DB 184 HLCVAGLEFGTAIVMYGPRHGSPEKQKYLFLFHSI 220

RESULT 7
US-08-467-947A-27
Sequence 27, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-947A-27

Query Match 37.7%; Score 311; DB 3; Length 222;
Best Local Similarity 38.9%; Pred. No. 2.6e-27;
Matches 61; Conservative 36; Mismatches 60; Indels 0; Gaps 0;

QY 1 VAICNPPLYPMVMSNKLQAQLLSISYVIGFLPLVHVSLLRLTFCRPNIIHYFCETIQ 60
DB 64 VAICHPRLYSALMSRVCSTMAVTSMIIIGVLSLHLVLLPLPFCVSKVNHFFCEITA 123
QY 61 LKTSICNGPSINALIIFIFGAFIOIPLMTIISYTRYVLEDILKKSEKRSKAFSTCGA 120
DB 124 ILKLACADTHLENMTVLGAVSVLGPFSSTIVSYACILGAILKIOSHEGOKRAKAFSTCSS 183
QY 121 HLTSVSLYGTILFMVYRPPASGLAEDODKYSLPFTI 157
DB 184 HLCVAGLEFGTAIVMYGPRHGSPEKQKYLFLFHSI 220

RESULT 8
US-08-118-270-68
Sequence 68, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:

Matches 58; Conservative 38; Mismatches 65; Indels 0; Gaps 0;

OY 2 AICNPPLYVWMSNKSQAOLLSISYVIGFLHPLVHVSLLRLTFECRFNIHYFCEIQL 61
 Db 125 AICHPRLRYTNLMSPKICGLMTAFSMILGSDGIIYAVATFSPFCGSRRLAHFCELP 184
 OY 62 FKISCNQPSINALIIFIGAFIOIPLMTIISYTRVLPDIILKKSEKGRSAFSTCGA 121
 Db 185 LILSCNDTSIFEKVFICSIYMLVFPVAILIASYAGVILAVIMGSGEGRRKAFSTCSSH 244
 OY 122 LLSVSLYGTILFMVYRPAASGLAEDDDKYSLFTIIPLL 162
 Db 245 LHWVMEYAGLFLWYIQPTSDRSPDRLVSVFTILTFL 285

RESULT 11

US-08-465-980-3
 ; Sequence 3, Application US/08465980
 ; Patent No. 5756309
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet, Daniel R.
 ; APPLICANT: LI, YI
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; ADDRESSEE: STUART & OLSTEIN
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/465,980
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-446
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 247 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-465-980-3

Query Match 35.5%; Score 293; DB 1; Length 247;
 Best Local Similarity 43.6%; Pred. No. 3e-25;
 Matches 58; Conservative 27; Mismatches 48; Indels 0; Gaps 0;

OY 1 VAICNPPLYVWMSNKSQAOLLSISYVIGFLHPLVHVSLLRLTFECRFNIHYFCEIQL 60
 Db 113 VAICFPLHYTAISPMICLALVALSWLTFPHAMHTLLMARLCFCADVNIPIHFCDMSA 172
 OY 61 LFKISCNQPSINALIIFIGAFIOIPLMTIISYTRVLPDIILKKSEKGRSAFSTCGA 120
 Db 173 LKLAFSDTRVNMWVIFIMGGLIVIPFLILLSYARIYSSILKVPSSKIGCKAFSTCGS 232
 OY 121 HLSVSLYGTILI 133

Db 233 HLSVSLYGTIV 245

RESULT 12

US-09-053-303-3
 ; Sequence 3, Application US/09053303
 ; Patent No. 594890
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet, Daniel R.
 ; APPLICANT: LI, YI
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; ADDRESSEE: STUART & OLSTEIN
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/053,303
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/465,980
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-446
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 247 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-053-303-3

Query Match 35.5%; Score 293; DB 2; Length 247;
 Best Local Similarity 43.6%; Pred. No. 3e-25;
 Matches 58; Conservative 27; Mismatches 48; Indels 0; Gaps 0;

OY 1 VAICNPPLYVWMSNKSQAOLLSISYVIGFLHPLVHVSLLRLTFECRFNIHYFCEIQL 60
 Db 113 VAICFPLHYTAISPMICLALVALSWLTFPHAMHTLLMARLCFCADVNIPIHFCDMSA 172
 OY 61 LFKISCNQPSINALIIFIGAFIOIPLMTIISYTRVLPDIILKKSEKGRSAFSTCGA 120
 Db 173 LKLAFSDTRVNMWVIFIMGGLIVIPFLILLSYARIYSSILKVPSSKIGCKAFSTCGS 232
 OY 121 HLSVSLYGTILI 133
 Db 233 HLSVSLYGTIV 245

RESULT 13

PCT-US95-07093-3
 ; Sequence 3, Application PC/TUS9507093
 ; GENERAL INFORMATION:

APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 335800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07093-3

Query Match 35.5%; Score 293; DB 5; Length 247;
Best Local Similarity 43.6%; Pred. No. 3e-25; Mismatches 48; Indels 0; Gaps 0;
Matches 58; Conservative 27; Mismatches 48; Indels 0; Gaps 0;

QY 1 VAICNPPLYPVMSNKLISQALISIVIGFHLPLVHVSLLRLTFCRFNIHYFCEILQ 60
DB 113 VAICPPLHYTALMSPLCLALVALSVLTFPHAMLTLLMARLCLFCADNVIRHFFCDMSA 172

QY 61 LFKISGNSINALIIFIFGAFIQIPLMTIISTRVLPDLKKSEKRSKASTGCA 120
DB 173 LKLAESDRVNEWVIFWGLIIVIPILLIGSYARIIVSILKVPSSKIGICKASTGCS 232

QY 121 HLLSVLYGFTLI 133
DB 233 HLSVSLFPGTYI 245

RESULT 14
US-08-118-270-69
Sequence 69, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-69

Query Match 35.3%; Score 291; DB 1; Length 274;
Best Local Similarity 41.0%; Pred. No. 5.8e-25;
Matches 66; Conservative 36; Mismatches 49; Indels 10; Gaps 5;

QY 1 VAICNPPLYPVMSNKLISQALISIVIGFHLPLVHVSLLRLTFCRFNIHYFCEILQ 60
DB 96 VAICPPLHYTALMSPLCLALVALSVLTFPHAMLTLLMARLCLFCADNVIRHFFCDISP 152

QY 61 LFKISGNSINALIIFIFGAFIQIPLMTIISTRVLPDLKKSEKRSKASTGCA 120
DB 153 LKLSGSDRVNEWVIFLGLVIVIPVL-IIVSYARVASILKVPSSKIGICKASTGCS 210

QY 121 HLLSVLYGFTLIEMVVRPASGLAEDQDKVSLFTYIILPL 161
DB 211 HLSVSLFPGTYIIGLYLCPSSANSTVKEVL-----TVVPL 246

RESULT 15
PCT-US93-08528-69
Sequence 69, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993

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OM protein - protein search, using sw model

Run on: June 27, 2002, 13:12:38 ; Search time 42.96 Seconds
(without alignments)
362.348 Million cell updates/sec

Title: US-09-747-155-225

Sequence: 1 VAICNPILLYPYWMSNKLISAQ.....LAEDQKYSLEFYTIIPLL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	385	46.7	304	2 S29709	olfactory receptor
2	382	46.3	157	2 S58020	probable olfactory
3	382	46.3	309	1 S51356	olfactory receptor
4	371	45.0	157	2 S58017	probable olfactory
5	362	43.9	157	2 S57998	probable olfactory
6	360	43.6	314	2 A37286	olfactory receptor
7	358	43.4	157	2 S58038	probable olfactory
8	356	43.2	315	2 JCS201	chemoreceptor TB56
9	345	41.8	314	2 S29707	olfactory receptor
10	344	41.7	161	2 A40745	odorant receptor (
11	343	41.6	157	2 S58014	probable olfactory
12	342.5	41.5	313	2 S20571	olfactory receptor
13	341	41.3	157	2 S58007	probable olfactory
14	340	41.2	305	2 S29711	olfactory factor O
15	339	41.1	157	2 S58000	probable olfactory
16	338	41.0	315	2 JCS458	olfactory receptor
17	337	40.8	2	138480	olfactory receptor
18	337	40.8	314	2 H23701	olfactory receptor
19	336	40.7	312	2 I23701	olfactory receptor
20	335	40.6	157	2 S58018	probable olfactory
21	334	40.5	312	2 S29708	olfactory receptor
22	334	40.5	314	2 S20572	olfactory receptor
23	333	40.4	2	558030	probable olfactory
24	332	40.2	216	2 I38476	olfactory receptor
25	331	40.1	225	2 I38478	olfactory receptor
26	329	39.9	310	2 E23701	olfactory receptor
27	328	39.8	216	2 I38474	probable olfactory
28	326.5	39.6	158	2 S58016	probable olfactory
29	326	39.5	157	2 S58026	probable olfactory

30	324	39.3	157	2 S58024	probable olfactory
31	324	39.3	216	2 I38470	olfactory receptor
32	322.5	39.1	156	2 S58072	probable olfactory
33	320	38.8	157	2 S58034	probable olfactory
34	320	38.8	216	2 I38479	olfactory receptor
35	318	38.5	157	2 S58027	probable olfactory
36	316	38.3	157	2 S57999	probable olfactory
37	316	38.3	312	2 G23701	olfactory receptor
38	313	37.9	157	2 S58068	probable olfactory
39	311	37.7	216	2 I38477	olfactory receptor
40	311	37.7	222	2 D40745	odorant receptor (
41	310	37.6	311	2 JCS200	chemoreceptor TB3
42	310	37.6	313	2 B23701	olfactory receptor
43	310	37.6	318	2 JCS202	chemoreceptor TB64
44	309	37.5	157	2 S57996	probable olfactory
45	308.5	37.4	312	2 A48413	probable olfactory

ALIGNMENTS

RESULT 1
S29709
Olfactory receptor OR14 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
R:Accession: S29709
R:Rattus, K.; Krieger, J.; Strotmann, J.; Boehhoff, I.; Kubick, S.; Baumstark, C.; Br
Nature 361, 353-356, 1993
A:Title: Cloning and expression of odorant receptors.
A:Reference number: S29707; MUID:93149273
A:Accession: S29709
A:Molecule type: mRNA
A:Residues: 1-304 <RAM>
C:Superfamily: olfactory receptor OR14

Query Match 46.7%; Score 385; DB 2; Length 304;

Best Local Similarity 48.5%; Pred. No. 3.8e-31;
Matches 79; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 VAICNPILLYPYWMSNKLISAQSLISYVIGFLPLVHVSLLRLTPCRNRIHYFCEILQ 60
DB 117 VAICNPILLYPYWMSNKLISAQSLISYVIGFLPLVHVSLLRLTPCRNRIHYFCEILP 176
QY 61 LFKISCPSPINALIIFFGAF-IOIPLMTIISYTVLFDILKKSEKRSKAFSTCG 119
DB 177 LLELSCNSTFNEIIVFIVVAIDIVP-IVSIFISYALILSLRMHSTEGRSKAFSTCS 235
QY 120 AHLISVSLYGTLLIFMYRPAAGLAEDQKYSLEFYTIIPLL 162
DB 236 SHLIYVCLLFSGAFMYLKLPSILPLDQKVSLEFYTIIPVWL 278

RESULT 2

S58020
Probable olfactory receptor tpcr09 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999

C:Accession: S58020

R:Vanderhaeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
submitted to the EMBL Data Library, July 1995

A:Description: Male germ cells from several mammalian species express a specific repe

A:Reference number: S57995

A:Accession: S58020

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-157 <VAN>

A:Cross-references: EMBL:X89681; NID:9902351; PIDD:CA61828.1; PTD:9902352

C:Superfamily: olfactory receptor OR14

Query Match 46.3%; Score 382; DB 2; Length 157;

RESULT 14

S29711

Olfactory factor OR37 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998

C:Accession: S29711

R:Ramling, K.; Krieger, J.; Strommann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Bredt

Nature 361, 353-356, 1993

A:Title: Cloning and expression of odorant receptors.

A:Reference number: S29707; MUID:93149273

A:Accession: S29711

A:Molecule type: mRNA

A:Residues: 1-305 <RAM>

C:Superfamily: Olfactory receptor OR14

Query Match

41.2%; Score 340; DB 2; Length 305;

Best Local Similarity 41.4%; Pred. No. 1.3e-26;

Matches 70; Conservative 34; Mismatches 57; Indels 8; Gaps 3;

QY 1 VAICNPPLYPVMSNKLISQQLISIVIGFLHPLVHSLRLKLTFCRNIHIFYCETLQ 60

DB 112 VAICNPPLRYSVTMSKEVYVMSASWFSGINSVQTSIAMRLPFCGNVNHFTCEVLA 171

QY 61 LEKISCNPSINALIIFIRG-AFIOIPTLTIISYTRVLFDILKKSEKSKAFSTCG 119

DB 172 VKIKCADISLNIYVVISNMAFLVP-LLIFSVILITVTLRMSASGRKRKAFSTCS 230

QY 120 AHLTSVSLYGTLLIFMYVPAS-----GLAEDODKVSLSFYIIIPLL 162

DB 231 AHLTVVVFYGTIFSMYAKPKSDLTGKDKFQTSKIIISLFGVYTPML 279

RESULT 15

S58000

Probable olfactory receptor tpcr71 - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 03-Nov-2000

C:Accession: S58000

R:Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentier, M.

submitted to the EMBL Data Library, July 1995

A:Description: Male germ cells from several mammalian species express a specific repertoire

A:Reference number: S57995

A:Accession: S58000

A:Status: Preliminary

A:Molecule type: mRNA

A:Cross-references: EMBL:X89663; NID:g902194; PIDN:CAA61810.1; PID:g902195

C:Superfamily: Olfactory receptor OR14

Query Match

41.1%; Score 339; DB 2; Length 157;

Best Local Similarity 43.2%; Pred. No. 8.2e-27;

Matches 67; Conservative 34; Mismatches 54; Indels 0; Gaps 0;

QY 3 ICNPLLYPVMNSKLSAQLISIVIGFLHPLVHSLRLKLTFCRNIHIFYCETLQ 62

DB 1 ICHPLHYSVIMSWRCVQAVTSMAGSLLALVHLILRLPFCGPHETNHFFCETLSVL 60

QY 63 KISCNPSINALIIFIRGAFIOIPTLTIISYTRVLFDILKKSEKSKAFSTCGAHL 122

DB 61 KIACADTRINOVVIFRNASVILVGPLCLVVSRLFAILRIQSGEGRKRAFSTCSSHL 120

QY 123 LSVSLYGTLLIFMYVPASGLAEDODKVSLSFYTI 157

DB 121 CVVGLFSGSAIVMYMAPKSNHPEOQKIISLFSYL 155

Search completed: June 27, 2002, 14:04:46

Job time: 3128 sec

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FT TRANSMEM 272 292 7 (POTENTIAL).
 FT DOMAIN 293 312 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 97 179 BY SIMILARITY.
 SQ SEQUENCE 312 AA; 35093 MW; BA893613AC929BC1 CRC64;

Query Match 50.2%; Score 414; DB 1; Length 312;
 Best Local Similarity 45.1%; Pred. No. 1.2e-11;
 Matches 73; Conservative 47; Mismatches 42; Indels 0; Gaps 0;

QY 1 VAICNPILLYVWMSNKLISAQLSIVYIGFLHPLVHSLRLTFGRNIIHYFCIQL 60
 |||||
 DB 124 VAICKPLLYPSTMTKAVCMRWLVKGLVSLAFNLVHTSGLLKLSFCCSNVNVNHFCDNSP 183
 -61 LFKISGNPSINALIFIFGAFIOPIPLMTIISYTRVLEDDIKKSEKSKAFSTCGA 120
 |||||
 DB 184 LFOISSSTLNLNLFVIFGSLFVMSIITILLSYVFIITLVVIRKSKDKYAFSTCTS 243
 |||||
 QY 121 HLISVSLYGTILFMYVVPASGLAEDODKYSLFYITIIPL 162
 |||||
 DB 244 HLMAVSLFHGTIVMYLRPYKLFSLDTKIASLFYVIVPML 285

RESULT 2

ID OLF6_CHICK STANDARD; PRT; 312 AA.

AC P37072; Q98912;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Olfactory receptor-like protein COR6.
 GN COR6.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Olfactory epithelium;
 RX MEDLINE=96317247; PubMed=8734500;
 RA Nef S., Allaman I., Fiumelli H., de Castro E., Nef P.;
 RT "Olfaction in birds: differential embryonic expression of nine
 putative odorant receptor genes in the avian olfactory system.";
 RL Mech. Dev. 55:65-77(1996).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z79590; CAB01851.1; -
 CC GCRDB: GCR_1092; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00245; OLFACROR.
 DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; FALSE_NEG.
 DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Olfaction; Multigene family.
 FT DOMAIN 1 26
 FT TRANSMEM 27 49
 FT DOMAIN 50 57
 FT TRANSMEM 58 79
 FT DOMAIN 80 100
 FT TRANSMEM 101 120

FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 164
 FT DOMAIN 165 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226
 FT TRANSMEM 227 239
 FT TRANSMEM 240 260
 FT TRANSMEM 261 271
 FT TRANSMEM 272 292
 FT DOMAIN 293 312
 FT CARBOHYD 5 5
 FT DISULFID 97 179
 SQ SEQUENCE 312 AA; 35179 MW; 56D164BF99D59EA9 CRC64;

Query Match 49.5%; Score 408; DB 1; Length 312;
 Best Local Similarity 43.5%; Pred. No. 4.3e-31;
 Matches 70; Conservative 51; Mismatches 40; Indels 0; Gaps 0;

QY 2 AICNPILLYVWMSNKLISAQLSIVYIGFLHPLVHSLRLTFGRNIIHYFCIQL 61
 |||||
 DB 125 AICKPLLYPAIMTKAVCMRWLVKGLVSLAFNLVHTSGLLKLSFCCSNVNVNHFCDNSP 184
 |||||
 QY 62 FKISGNPSINALIFIFGAFIOPIPLMTIISYTRVLEDDIKKSEKSKAFSTCGA 121
 |||||
 DB 185 FOISSSTLNLNLFVIFGSLFVMSIITILLSYVFIITLVVIRKSKDKYAFSTCTS 244
 |||||
 QY 122 LLSVSLYGTILFMYVVPASGLAEDODKYSLFYITIIPL 162
 |||||
 DB 245 LMAVSLFHGTIVMYLRPYKLFSLDTKIASLFYVIVPML 285

RESULT 3

ID OLF5_CHICK STANDARD; PRT; 312 AA.

AC P37071;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Olfactory receptor-like protein COR5.
 GN COR5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Olfactory epithelium;
 RX MEDLINE=96317247; PubMed=8734500;
 RA Nef S., Allaman I., Fiumelli H., de Castro E., Nef P.;
 RT "Olfaction in birds: differential embryonic expression of nine
 putative odorant receptor genes in the avian olfactory system.";
 RL Mech. Dev. 55:65-77(1996).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: Z79589; CAB01850.1; -
 CC GCRDB: GCR_1093; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00245; OLFACROR.
 DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW

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CC -----
CC EMBL: Z79585; CAB01846.1; -
CC GCRB; GCR_1097; -
CC InterPro: IP000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00245; OLFACTORYR.
CC PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
CC PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Olfaction; Multigene family.
CC
CC FT DOMAIN 1 26
CC FT TRANSMEM 27 49
CC FT DOMAIN 50 57
CC FT TRANSMEM 58 79
CC FT DOMAIN 80 100
CC FT TRANSMEM 101 120
CC FT DOMAIN 121 139
CC FT TRANSMEM 140 164
CC FT DOMAIN 145 165
CC FT TRANSMEM 206 226
CC FT DOMAIN 227 239
CC FT TRANSMEM 240 260
CC FT DOMAIN 261 271
CC FT TRANSMEM 272 292
CC FT DOMAIN 293 318
CC FT CARBOHYD 5 5
CC FT DISULFID 97 179
CC FT SEQUENCE 318 AA: 35757 MW: D5C72EBA043A962 CRC64;

Query Match 47.4%; Score 391; DB 1; Length 318;
Best Local Similarity 43.2%; Pred. No. 1.7e-29;
Matches 70; Conservative 46; Mismatches 46; Indels 0; Gaps 0;

QY 1 VAICNPPLYVPMNSKLSAQLSLISYIGFLHPLVHSLRLTFECFNTHFYECILQ 60
DB 124 VAICKPLLYPAIMTKAVCMRLVGLSLVFLANSLVHRCGLKLKLSFCYSNVNHFCDISP 183
QY 61 LFKISCGPSINMLIIFPGAFIQIPILMTIISYTVFLFDILKKSEKRSKAFSTCGA 120
DB 184 LFOISSSTLNEULVITSSLEFVMSIITLISYVFIILTVMIRSKDKYKAFSTCTS 243
QY 121 HLVSLSLYGTLLFMVVRPASGLAEDQKVSLEYTIIIPL 162
DB 244 HLMAVSLFHGTIVFMVRSVKFLSLDTDKIASLEYTVVIML 285

RESULT 6
OLFL_CHICK STANDARD; PRT; 312 AA.
AC P37068;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Olfactory receptor-like protein COR2.
CN COR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RA MEDLINE=96317247; PubMed=8734500;
RT Nef S., Allman I., Flumelli H., de Castro E., Nef P.;
RT "Olfaction in birds: differential embryonic expression of nine
RT putative odorant receptor genes in the avian olfactory system.";

RL Mech. Dev. 55:65-77(1996).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL: Z79588; CAB01849.1; -
CC GCRB; GCR_1099; -
CC InterPro: IP000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00245; OLFACTORYR.
CC PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
CC PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Olfaction; Multigene family.
CC
CC FT DOMAIN 1 26
CC FT TRANSMEM 27 49
CC FT DOMAIN 50 57
CC FT TRANSMEM 58 79
CC FT DOMAIN 80 100
CC FT TRANSMEM 101 120
CC FT DOMAIN 121 139
CC FT TRANSMEM 140 164
CC FT DOMAIN 145 165
CC FT TRANSMEM 206 226
CC FT DOMAIN 227 239
CC FT TRANSMEM 240 260
CC FT DOMAIN 261 271
CC FT TRANSMEM 272 292
CC FT DOMAIN 293 312
CC FT CARBOHYD 5 5
CC FT DISULFID 97 179
CC FT SEQUENCE 312 AA: 35255 MW: 3A4362DF2722770C CRC64;

Query Match 47.0%; Score 388; DB 1; Length 312;
Best Local Similarity 43.2%; Pred. No. 3.1e-29;
Matches 70; Conservative 46; Mismatches 46; Indels 0; Gaps 0;

QY 1 VAICNPPLYVPMNSKLSAQLSLISYIGFLHPLVHSLRLTFECFNTHFYECILQ 60
DB 124 VAICKPLLYPSIMTKAVCMRLVGLSLVFLANSLVHRTSGLLKLSFCSSNVNHFCDNRP 183
QY 61 LFKISCGPSINMLIIFPGAFIQIPILMTIISYTVFLFDILKKSEKRSKAFSTCGA 120
DB 184 LFOISSSTLNEULVITSSLEFVMSIITLISYVFIILTVMIRSKDKYKAFSTCTS 243
QY 121 HLVSLSLYGTLLFMVVRPASGLAEDQKVSLEYTIIIPL 162
DB 244 HLMAVSLFHGTIVFMVRSVKFLSLDTDKIASLEYTVVIML 285

RESULT 7
OLFL_CANFA STANDARD; PRT; 311 AA.
AC Q95154;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Olfactory receptor-like protein OLFL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.


```
RX MEDLINE-97008103; PubMed-8855279;
RA Issel-Tarver L., Rine J.;
RT "Organization and expression of canine olfactory receptor genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10897-10902(1996).
CC -!- FUNCTION: PUTATIVE ODORANT OR SPERM CELL RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U53679; AAB37239.1; -.
CC GCRDb: GCR_1192; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00245; OLFACTORR.
DR PROSITE: PS00237; G-PROTEIN_RECIP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECIP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 25 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 57 78 2 (POTENTIAL).
FT DOMAIN 79 99 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 100 119 3 (POTENTIAL).
FT DOMAIN 120 138 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 139 157 4 (POTENTIAL).
FT DOMAIN 158 195 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 196 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 236 259 6 (POTENTIAL).
FT DOMAIN 260 271 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 272 291 7 (POTENTIAL).
FT DOMAIN 292 311 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 311 AA; 35209 MW; 05A2132474F543A1 CRC64;

Query Match
Best Local Similarity 45.9%; Score 379; DB 1; Length 311;
Matches 71; Conservative 36; Mismatches 55; Indels 0; Gaps 0;

OY 1 VAICNPILLYPVMSNKLQAOLLSISYVIGFLPHLVHSLRLTFCRPNIIHYFCETIQ 60
DB 123 VAICNPILLYPVMSRGICVWLVISYIGNMSLVHTSFARILKCDKNVINHFCDLPP 182
OY 61 LEKISGNPSINALLIFFGAFIQIPLMTIIISYTRVLFIDILKKSEKSKASTGCA 120
DB 183 LKLSCTDTINEMLSLYGSSVEIFCFIVIVISYFILRSVLRIRSSSGRKRTSTCAS 242
OY 121 HLISVSLYGTILFIYVVRPAGSLAEDODKVSLEFIIIPLL 162
DB 243 HLTSVTIYOGTLFIYSRPSYLSYSPNFDKIISVFYIIFPVL 284

RESULT 8
OSIL_HUMAN
ID OSIL_HUMAN STANDARD; PRT; 314 AA.
AC 013606;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 511 (Olfactory receptor-like protein OLF1).
GN OSIL OR OLF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
```

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Issel-Tarver L., Rine J.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL: U56420; AAB01214.1; -.
CC GCRDb: GCR_1925; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00245; OLFACTORR.
DR PROSITE: PS00237; G-PROTEIN_RECIP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECIP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 29 51 1 (POTENTIAL).
FT DOMAIN 52 59 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 60 81 2 (POTENTIAL).
FT DOMAIN 82 102 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 103 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 207 5 (POTENTIAL).
FT TRANSSEM 208 228 6 (POTENTIAL).
FT DOMAIN 229 241 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 242 262 7 (POTENTIAL).
FT DOMAIN 263 273 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 274 294 7 (POTENTIAL).
FT DOMAIN 295 314 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 191 BY SIMILARITY.
FT CARBOHYD 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 314 AA; 36048 MW; 334BEBF3D9AD63 CRC64;

Query Match
Best Local Similarity 45.9%; Score 379; DB 1; Length 314;
Matches 72; Conservative 37; Mismatches 53; Indels 0; Gaps 0;

OY 1 VAICNPILLYPVMSNKLQAOLLSISYVIGFLPHLVHSLRLTFCRPNIIHYFCETIQ 60
DB 126 VAICNPILLYPVMSRGICVWLVISYIGNMSLVHTSFARILKCDKNVINHFCDLPP 185
OY 61 LEKISGNPSINALLIFFGAFIQIPLMTIIISYTRVLFIDILKKSEKSKASTGCA 120
DB 186 LKLSCTDTINEMLSLYGSSVEIFCFIIIIISYFILLSLVKIRSPSGRKRTSTCAS 245
OY 121 HLISVSLYGTILFIYVVRPAGSLAEDODKVSLEFIIIPLL 162
DB 246 HLTSVTIYOGTLFIYSRPSYLSYSPNFDKIISVFYIIFPVL 287

RESULT 9
OLF2_CANFA
ID OLF2_CANFA STANDARD; PRT; 311 AA.
AC 095155;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Olfactory receptor-like protein OLF2.
GN Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97008103; PubMed=8855279;
 RA Issel-Tarver L., Rine J.;
 RT "Organization and expression of canine olfactory receptor genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:10897-10902(1996).
 CC -1- FUNCTION: PUTATIVE ODORANT OR SPERM CELL RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: U53680; AAB37240.1; .
 DR GCRDB: GCR_1191; .
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR00245; OLEACTORR.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1;
 DR PROSITE: PS00262; G_PROTEIN_REC_P2.1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSMEM 26 49
 FT DOMAIN 50 57
 FT TRANSMEM 58 79
 FT DOMAIN 80 100
 FT TRANSMEM 101 120
 FT DOMAIN 121 139
 FT TRANSMEM 140 158
 FT DOMAIN 159 196
 FT TRANSMEM 197 219
 FT DOMAIN 220 236
 FT TRANSMEM 237 260
 FT DOMAIN 261 292
 FT TRANSMEM 293 311
 FT DOMAIN 311 311
 FT CARBOHYD N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 311 AA: 35177 MW: C57D24B3B48FAC20 CRC64;
 Query Match 45.3%; Score 374; DB 1; Length 311;
 Best Local Similarity 41.6%; Pred. No. 6, 3e-28;
 Matches 67; Conservative 43; Mismatches 51; Indels 0; Gaps 0;
 OY 2 AICNPPLLYPVMSNKLKSAQLLSISYVIGFLPHVLSLLRLFCRFNIIHYCELIQ 61
 DB 125 AISHPLLYVSMSSKCSLMLAGVYLVGLMDASVNTILTRLCFCSSNVTNHFCDVPL 184
 OY 62 FKISCGSPSINALIIF-IFGAFIQIPTLMTIISYTRVLFDLKKSEKSKAFSTCG 121
 DB 185 LLSCSDQVNELVFTIFGFIILITLSGLFVSCYIIILAVRKINSAGKFAFSTCTSH 244
 OY 122 LLSVSLYGLTIFMYVRPASGLAEDODKYVSLFTYTIIP 162
 DB 245 LTVAVIFOGTLMFMYRPSSSYSLLDDKIISLFLYSLVPM 285
 RESULT 10
 ODB8_HUMAN STANDARD; PRT; 311 AA.
 AC 015620;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 888 (Olfactory receptor TPCR85).

GN ORB8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 126-282 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97224452; PubMed=9119360;
 RA Vanderhaeghen P., Schumann S., Vassart G., Parmentier M.;
 RT "Specific repertoire of olfactory receptor genes in the male germ
 RT cells of several mammalian species.";
 RL Genomics 39:239-246(1997).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: X89675; CA61822.1; .
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1;
 DR PROSITE: PS00262; G_PROTEIN_REC_P2.1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSMEM 26 49
 FT DOMAIN 50 57
 FT TRANSMEM 58 79
 FT DOMAIN 80 100
 FT TRANSMEM 101 120
 FT DOMAIN 121 139
 FT TRANSMEM 140 158
 FT DOMAIN 159 195
 FT TRANSMEM 196 219
 FT DOMAIN 220 236
 FT TRANSMEM 237 259
 FT DOMAIN 260 272
 FT TRANSMEM 273 292
 FT DOMAIN 293 311
 FT DISULFID 97 189
 FT CARBOHYD N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 204 204 G -> S (IN REF. 1).
 SQ SEQUENCE 311 AA: 34482 MW: 9DB8AC4DA179ABE6 CRC64;
 Query Match 44.4%; Score 366; DB 1; Length 311;
 Best Local Similarity 44.8%; Pred. No. 3, 5e-27;
 Matches 73; Conservative 37; Mismatches 51; Indels 2; Gaps 2;
 OY 1 VAICNPPLLYPVMSNKLKSAQLLSISYVIGFLPHVLSLLRLFCRFNIIHYCELIQ 60
 DB 124 VAICNPPLLYPVMSNKLKSAQLLSISYVIGFLPHVLSLLRLFCRFNIIHYCELIQ 183
 OY 61 LFKISCGSPSINALIIF-IFGAFIQIPTLMTIISYTRVLFDLKKSEKSKAFSTCG 119
 DB 184 LFKISCGSPSINALIIF-IFGAFIQIPTLMTIISYTRVLFDLKKSEKSKAFSTCG 242
 OY 120 AHSLSVLYGLTIFMYVRPASGLAEDODKYVSLFTYTIIP 162
 DB 243 SHIAVSLFEGSGAFMYLKPFSLLAMNQGKVSFLFTYVPM 285
 RESULT 11
 ODB2_HUMAN

```

ID      08B2_HUMAN      STANDARD:      PRT:      311 AA.
AC      OGG2M5:
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Olfactory receptor 8D2 (Olfactory receptor-like protein JCG2).
GN      OR8D2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID:9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Tongue;
RA      Gaudin J.-C., Choibert J.-M., Haertle T.;
RT      "Molecular cloning of olfactory receptor-like mRNAs expressed in human
RT      tongue.";
RL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN THE TONGUE.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      -----
DR      EMBL; AF162668; AAC43386.1; -
DR      EMBL; AF162669; AAC43387.1; -
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PF00237; GPCR_RHODOPS.
DR      PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; FALSE_NEG.
DR      PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein;
KW      Multigene family; Olfaction.
FT      DOMAIN          1      25      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        26      49      1 (POTENTIAL).
FT      DOMAIN          50      57      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM        58      79      2 (POTENTIAL).
FT      DOMAIN          80      100     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        101      120     3 (POTENTIAL).
FT      DOMAIN          121      139     CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM        140      158     4 (POTENTIAL).
FT      DOMAIN          159      195     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        196      219     5 (POTENTIAL).
FT      DOMAIN          220      236     CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM        237      259     6 (POTENTIAL).
FT      DOMAIN          260      272     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        273      292     7 (POTENTIAL).
FT      DOMAIN          293      311     CYTOPLASMIC (POTENTIAL).
FT      DISULFID        97      189     BY SIMILARITY.
FT      CARBOHYD        5      5      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      311 AA; 34857 MW; ECE606FBBC962A82 CRC64;

```

Query Match 44.4%; Score 366; DB 1; Length 311;
Best Local Similarity 39.5%; Pred. NO. 3.5e-27;
Matches 64; Conservative 45; Mismatches 53; Indels 0; Gaps 0;

```

OY      1 VAICPPLLYPVMWSKSLAOLSLISYVGFPLPLVHSLSLATPCRFNLIHYFCETIQ 60
OY      ||||| |||| :|||::: :||| :||| || :|||::: :|||::: ||
Db      124 VAICPPLLYNYVMWSKSLAOLSLISYVGFPLPLVHSLSLATPCRFNLIHYFCETILP 183
OY      61 LFKISGCPNSINALITFGCAFIQPTLITLISYTRVLDFLLKKKSGKRSKAFSTGCA 120
OY      :||| :|||::: || :|||::: || :|||::: || :|||::: || :
Db      184 LFLTSCSFTSHINEILFLITGCVNLTATLAVLISVAFLFSSILGHSITGSGKATGTCS 243
OY      121 HLISVSLYGTILIMYVAPASGLAEDQKYSLFPTIIPL 162

```

[illegible]

QY 61 LKISCGPSINALIFIFGAFIPIPTMTIISYRVLEFDILKKSEKRSKASTCGA 120
 DB 184 LKLSGSDPHNEVLVFMVGLVIVIPFVLLIYSARVASILKVSXGINKHIFSTGCS 243
 QY 121 HLTSVLYGTGLFMVYRPAAGLAEDODKXYSLEFYITIIPL 162
 DB 244 HLTSVLYGTGLFMVYRPAAGLAEDODKXYSLEFYITIIPL 162

RESULT 13
 OFS1_HUMAN STANDARD: PRT; 314 AA.

AC 095221;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 5f1 (Olfactory receptor 11-10) (OR11-10).
 OS OR5F1.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBL_TaxID=9606;

SEQUENCE OF 68-283 FROM N.A.
 MEDLINE:99005533; PubMed:9787077;
 Buettner J.A., Glusman G., Ben-Arie N., Ramos P., Lancel D.,
 Evans G.A.;
 "Organization and evolution of olfactory receptor genes on human
 chromosome 11.";
 Genomics 53:56-68(1998).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL: AF065863; AAC70017.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
 DR PROSITE: PS00262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSSEM 26 49
 FT DOMAIN 50 57
 FT TRANSSEM 58 79
 FT DOMAIN 80 100
 FT TRANSSEM 101 120
 FT DOMAIN 121 139
 FT TRANSSEM 140 158
 FT DOMAIN 159 195
 FT TRANSSEM 196 219
 FT DOMAIN 220 236
 FT TRANSSEM 237 259
 FT DOMAIN 260 272
 FT TRANSSEM 273 292
 FT DOMAIN 293 314
 FT DISULFID 97 189
 FT CARBOHYD 5
 FT SEQUENCE 314 AA; 35131 MW; C14A9A335CD76E3A3 CRC64;

Query Match 42.18; Score 347; DB 1; Length 314;
 Best Local Similarity 41.0%; Pred. No. 2.1e-25.

Matches 66; Conservative 39; Mismatches 56; Indels 0; Gaps 0;

QY 2 AICNPLLYVWMSNKNKADLLSYISYIGFLHPLVSLRLTFPCFENIHYFYCEIQL 61
 DB 125 AICRPLLYSLIMSRYLYLMAAGAFAGLNEVNSHWSLSFCSNVIHIFFCOSPL 184
 QY 62 FKISCGPSINALIFIFGAFIPIPTMTIISYRVLEFDILKKSEKRSKASTCGA 121
 DB 185 FKLSGSDPHNEVLVFMVGLVIVIPFVLLIYSARVASILKVSXGINKHIFSTGCS 244
 QY 122 HLTSVLYGTGLFMVYRPAAGLAEDODKXYSLEFYITIIPL 162
 DB 245 HLTSVLYGTGLFMVYRPAAGLAEDODKXYSLEFYITIIPL 162

RESULT 14
 OFS3_HUMAN STANDARD: PRT; 315 AA.

AC P47888; Q9UBE7; Q9PIQ4;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 3a3 (Olfactory receptor 17-201) (OR17-201).
 OS OR3A3.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBL_TaxID=9606;

SEQUENCE FROM N.A.
 MEDLINE:20139433; PubMed:10673334;
 Glusman G., Sosinsky A., Ben-Asher E., Avidan N., Sonkin D., Bahar A.,
 Rosenthal A., Clifton S., Roe B., Ferraz C., Demallie J.G., Lancel D.;
 "Sequence, structure, and evolution of a complete human olfactory
 RT receptor gene cluster.";
 RT Genomics 63:227-245(2000).
 RN [3]
 RN SEQUENCE OF 71-286 FROM N.A.
 RN MEDLINE:94272458; PubMed:8004088;
 RN Ben-Arie N., Lancel D., Taylor C., Khen M., Walker N.,
 RA Ledbetter D.H., Carozzo R., Patel K., Sheer D., Lehnach H.,
 RA North M.A.;
 "Olfactory receptor gene cluster on human chromosome 17: possible
 RT duplication of an ancestral receptor repertoire.";
 RT Hum. Mol. Genet. 3:229-235(1994).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL: AF095725; AAF03262.1; ALT_INT.
 DR EMBL: AF087926; AAF37316.1;
 DR EMBL: U76377; AAD00250.1;
 DR EMBL: U78308; AAD00277.1;
 DR EMBL: U04688; AAA1851.1;
 DR GCRDB: GCR_0855;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
 DR PROSITE: PS00262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family: Olfaction.
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 52 1 (POTENTIAL).
FT DOMAIN 53 60 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 61 82 2 (POTENTIAL).
FT DOMAIN 83 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 123 3 (POTENTIAL).
FT DOMAIN 124 142 4 (POTENTIAL).
FT TRANSMEM 144 161 5 (POTENTIAL).
FT DOMAIN 162 199 6 (POTENTIAL).
FT TRANSMEM 200 222 7 (POTENTIAL).
FT DOMAIN 223 239 8 (POTENTIAL).
FT TRANSMEM 240 262 9 (POTENTIAL).
FT DOMAIN 263 275 10 (POTENTIAL).
FT TRANSMEM 276 295 11 (POTENTIAL).
FT DOMAIN 296 315 12 (POTENTIAL).
FT DISULFID 100 192 13 (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 165 165 A -> G (IN REF. 3).
FT CONFLICT 183 183 D -> E (IN REF. 3).
FT CONFLICT 187 187 L -> V (IN REF. 3).
SQ SEQUENCE 315 AA: 34275 MW: 69B976A0FF80CCDA CRC64.

Query Match 41.9%; Score 346; DB 1; Length 315;
Best Local Similarity 39.5%; Pred. No. 2.6e-25;
Matches 64; Conservative 38; Mismatches 60; Indels 0; Gaps 0;

QY 1 VAICNPDLTPVPMNSKLSAQLSISVIGFLHPLVHVSLLRLTFGRNIIHYFCEIIQ 60
DB 127 LAICOPPLVSTMSQTVQHMVAASWACAFNALHTVAMSTLNEFGPNEVNHFYCDLPQ 186
QY 61 LKISGNGSINALIIFIGAFIQPTLTIIISYRVLFEDILKKSEGRSAFTCGA 120
DB 187 LKLSGNGSINALIIFIGAFIQPTLTIIISYRVLFEDILKKSEGRSAFTCGA 246
QY 121 HLTVSLYGYTLIFMYVRPASGLAEDODKRVSLFYTIIPLL 162
DB 247 HLTVGYIFGYGVFSYMRGSSVSSDKDGVGVMTVINPML 288

RESULT 15
OSVL_HUMAN STANDARD; PRT; 321 AA.
ID OSVL_HUMAN
AC 090GF6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 5V1 (Hs6M1-21).
GN OR5V1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tracey A.;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AL096770; CAB65797.1; -
CC DR InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family: Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 2 (POTENTIAL).
FT TRANSMEM 58 79 3 (POTENTIAL).
FT DOMAIN 80 100 4 (POTENTIAL).
FT TRANSMEM 101 120 5 (POTENTIAL).
FT DOMAIN 121 139 6 (POTENTIAL).
FT TRANSMEM 140 158 7 (POTENTIAL).
FT DOMAIN 159 195 8 (POTENTIAL).
FT TRANSMEM 196 219 9 (POTENTIAL).
FT DOMAIN 220 236 10 (POTENTIAL).
FT TRANSMEM 237 259 11 (POTENTIAL).
FT DOMAIN 260 272 12 (POTENTIAL).
FT TRANSMEM 273 292 13 (POTENTIAL).
FT DOMAIN 293 321 14 (POTENTIAL).
FT DISULFID 97 189 15 (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 321 AA: 36056 MW: AAC426DFCF58E375 CRC64.

Query Match 41.9%; Score 346; DB 1; Length 321;
Best Local Similarity 42.0%; Pred. No. 2.6e-25;
Matches 68; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

QY 1 VAICNPDLTPVPMNSKLSAQLSISVIGFLHPLVHVSLLRLTFGRNIIHYFCEIIQ 60
DB 124 LAICNPDLTPVPMNSKLSAQLSISVIGFLHPLVHVSLLRLTFGRNIIHYFCEIIQ 183
QY 61 LKISGNGSINALIIFIGAFIQPTLTIIISYRVLFEDILKKSEGRSAFTCGA 120
DB 184 LKLSGNGSINALIIFIGAFIQPTLTIIISYRVLFEDILKKSEGRSAFTCGA 243
QY 121 HLTVSLYGYTLIFMYVRPASGLAEDODKRVSLFYTIIPLL 162
DB 244 HLTVGYIFGYGVFSYMRGSSVSSDKDGVGVMTVINPML 285

Search completed: June 27, 2002, 14:11:27
Job time: 459 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2002, 14:03:03 ; Search time 66.28 Seconds
(without alignments)
422.830 Million cell updates/sec

Title: US-09-747-155-225
Perfect score: 825
Sequence: 1 VAICNPILLYVMMSNKLQAQ.....LAEDQKVSLSFYITIIPL 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	ID	Description
1	825	100.0	162 4 Q9NZP5	Q9NZP5 homo sapien
2	806	97.7	162 6 Q9N1M1	Q9N1M1 pan troglod
3	562	68.1	221 11 Q9Z231	Q9Z231 rattus norv
4	527	63.9	162 6 Q9N1M4	Q9N1M4 papio hamad
5	403	48.8	268 11 Q9ERX2	Q9ERX2 mus musculu
6	400	48.5	312 13 Q9O807	Q9O807 gallus galli
7	395	47.9	308 11 Q9EOA0	Q9EOA0 mus musculu
8	393	47.6	223 11 Q9Z1V5	Q9Z1V5 mus musculu
9	393	47.6	314 11 Q9EOB8	Q9EOB8 mus musculu
10	389	47.2	310 11 Q9EOA7	Q9EOA7 mus musculu
11	387	46.9	221 11 Q9Z230	Q9Z230 rattus norv
12	387	46.9	310 11 Q9EOB0	Q9EOB0 mus musculu
13	385	46.7	304 11 Q9O836	Q9O836 rattus sp.
14	382	46.3	157 11 Q62345	Q62345 mus musculu
15	382	46.3	309 11 Q63395	Q63395 rattus norv
16	380	46.1	158 13 Q42214	Q42214 neoturus ma

17	380	46.1	217 4 Q96RC7	Q96RC7 homo sapien
18	380	46.1	313 6 Q77758	Q77758 hylobates 1
19	379.5	46.0	314 11 Q9EOA5	Q9EOA5 mus musculu
20	378.5	45.9	309 11 Q9EOA6	Q9EOA6 mus musculu
21	378	45.8	162 6 Q9N1N3	Q9N1N3 papio hamad
22	377	45.7	308 11 Q9EO98	Q9EO98 mus musculu
23	377	45.7	223 11 Q9Z1U7	Q9Z1U7 mus musculu
24	377	45.7	268 11 Q9ERX3	Q9ERX3 rattus norv
25	377	45.7	308 11 Q9EO99	Q9EO99 mus musculu
26	375.5	45.5	309 11 Q9EOA4	Q9EOA4 mus musculu
27	374	45.3	311 11 Q9EOB4	Q9EOB4 mus musculu
28	374	45.3	332 13 Q9O806	Q9O806 gallus galli
29	373	45.2	216 4 Q96RB2	Q96RB2 homo sapien
30	372	45.1	176 6 Q77545	Q77545 sus scrofa
31	371.5	45.0	309 11 Q9EOA8	Q9EOA8 mus musculu
32	371	45.0	157 4 Q15617	Q15617 homo sapien
33	370	44.8	162 6 Q9N1G2	Q9N1G2 salmtril bol
34	370	44.8	216 4 Q96RC2	Q96RC2 homo sapien
35	369	44.7	311 11 Q9EOA3	Q9EOA3 mus musculu
36	369	44.7	314 6 Q77756	Q77756 pan troglod
37	368	44.6	318 11 Q9OY00	Q9OY00 mus musculu
38	367.5	44.5	215 4 Q96RD0	Q96RD0 homo sapien
39	367	44.5	237 11 Q9ROG3	Q9ROG3 marmota mar
40	367	44.5	312 13 Q9O808	Q9O808 gallus galli
41	365.5	44.3	217 4 Q96RC3	Q96RC3 homo sapien
42	364	44.1	162 6 Q9N1H0	Q9N1H0 salmtril scl
43	364	44.1	217 4 Q96RA9	Q96RA9 homo sapien
44	364	44.1	312 11 Q9EOB1	Q9EOB1 mus musculu
45	362	43.9	157 6 Q28307	Q28307 canis fam11

ALIGNMENTS

RESULT 1
ID Q9NZP5 PRELIMINARY; PRT; 162 AA.
AC Q9NZP5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-JUN-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
GN HSA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Roudier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
DR EMBL: AF179759; AAF40348.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1, 1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 162 162
SQ SEQUENCE 162 AA; 18386 MW; 6716C48C3ED0E4D8 CRC64;

Query Match 100.0%; Score 825; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 1, 1e-77;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAICNPILLYVMMSNKLQAQLSISYIGFLPHLVHVSLLRLTFQCFNIIHYFCIIQ 60
DB 1 VAICNPILLYVMMSNKLQAQLSISYIGFLPHLVHVSLLRLTFQCFNIIHYFCIIQ 60
QY 61 LFRISCGPSINLLIFIFGAFIQIPIIMTIIISYRVLRLDLKKSEKRSKAFSPGCA 120

```

|||||
Db 61 LFKISCNPSINALIIFFGAFIQIPLMTIIISTRLVFLPILKKSEKSKAFSTCGA 120
OY 121 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 162
Db 121 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 162

RESULT 2
O9N1M1 PRELIMINARY: PRT: 162 AA.
ID O9N1M1
AC O9N1M1: 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
GN PTR210.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
DR EMBL: AF179735; AAF40330.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PR00001; 7tm_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW Receptor.
FT NON_TER 1 162
FT NON_TER 162 162
SQ SEQUENCE 162 AA; 18389 MW; 586280CC7BD5FACE CRC64;

Query Match 97.7%; Score 806; DB 6; Length 162;
Best Local Similarity 97.5%; Pred. No. 1e-75; 2; Indels 0; Gaps 0;
Matches 158; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VAICNPPLYVPMNSNKLISQALISYVIGFLPVLVHSLRLFCRNIIHYFCETLQ 60
Db 1 VAICNPPLYVPMNSNKLISQALISYVIGFLPVLVHSLRLFCRNIIHYFCETLQ 60
OY 61 LFKISCNPSINALIIFFGAFIQIPLMTIIISTRLVFLPILKKSEKSKAFSTCGA 120
Db 61 LFKISCNPSINALIIFFGAFIQIPLMTIIISTRLVFLPILKKSEKSKAFSTCGA 120
OY 121 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 162
Db 121 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 162

RESULT 3
O9N231 PRELIMINARY: PRT: 221 AA.
ID O9N231
AC O9N231: 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HFV-FDI;
RA Singer M.S., Hughes T.E., Shepherd G.M., Greer C.A.;
RT "Isolation of olfactory receptor mRNA sequences from olfactory bulb
RT glomerular layer.";

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Submitted (SFP-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF091575; AAC64595.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 221 AA; 25000 MW; 73C05CA5318E5DE CRC64;

Query Match 68.1%; Score 562; DB 11; Length 221;
Best Local Similarity 65.2%; Pred. No. 2.3e-50;
Matches 105; Conservative 25; Mismatches 31; Indels 0; Gaps 0;

OY 1 VAICNPPLYVPMNSNKLISQALISYVIGFLPVLVHSLRLFCRNIIHYFCETLQ 60
Db 61 VAICNPPLYVPMNSNKLISQALISYVIGFLPVLVHSLRLFCRNIIHYFCETLQ 60
OY 61 LFKISCNPSINALIIFFGAFIQIPLMTIIISTRLVFLPILKKSEKSKAFSTCGA 120
Db 61 LFKISCNPSINALIIFFGAFIQIPLMTIIISTRLVFLPILKKSEKSKAFSTCGA 120
OY 121 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 161
Db 121 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 161
OY 181 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 221
Db 181 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 221

RESULT 4
O9N1M4 PRELIMINARY: PRT: 162 AA.
ID O9N1M4
AC O9N1M4: 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
GN PPA138.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
DR EMBL: AF179721; AAF40317.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW Receptor.
FT NON_TER 1 162
FT NON_TER 162 162
SQ SEQUENCE 162 AA; 18112 MW; ACD9BA1ECBD37959 CRC64;

Query Match 63.9%; Score 527; DB 6; Length 162;
Best Local Similarity 62.3%; Pred. No. 7e-47;
Matches 101; Conservative 22; Mismatches 39; Indels 0; Gaps 0;

OY 1 VAICNPPLYVPMNSNKLISQALISYVIGFLPVLVHSLRLFCRNIIHYFCETLQ 60
Db 1 VAICNPPLYVPMNSNKLISQALISYVIGFLPVLVHSLRLFCRNIIHYFCETLQ 60
OY 61 LFKISCNPSINALIIFFGAFIQIPLMTIIISTRLVFLPILKKSEKSKAFSTCGA 120
Db 61 LFKISCNPSINALIIFFGAFIQIPLMTIIISTRLVFLPILKKSEKSKAFSTCGA 120
OY 121 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 162
Db 121 HLTSVSLYGTLEFMYVRPASGLAEDODKYSLEFYTIIPLL 162

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Db 121 HLFSVCLYVGLPLFMVYVGPASPOADDQDQWECVYTVIIPFL 162

RESULT 5

Q9ERX2 PRELIMINARY; PRT; 268 AA.

AC Q9ERX2; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RM NCB1_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-TESTIS;

RX MEDLINE-20469363; PubMed-11014824;

RA Branscomb A., Seger J., White R.L.;

RL "Evolution of odorant receptors expressed in mammalian testes.";

RT Genetics 156:785-797(2000).

DR EMBL; AF21049; AAG21322.1; -

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCR_RHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.

KW Receptor.

FT NON_TER

FT NON_TER

SO SEQUENCE 268 AA; 29757 MW; F7AAE1764094E78C CRC64;

Query Match 48.8%; Score 403; DB 11; Length 268;

Best Local Similarity 42.0%; Pred. No. 7.6e-34;

Matches 68; Conservative 47; Mismatches 47; Indels 0; Gaps 0;

OY 1 VAICNPPLLYVWMSNKLISAOQLSISYVIGFLHPLVHVSLLRLTFRCFNIIHYFCEIQ 60

Db 100 VAICRPLLYVWMSNKLISAOQLSISYVIGFLHPLVHVSLLRLTFRCFNIIHYFCEIQ 159

OY 61 LFKISCGPSINALIIFFGAFIQIPLMTIISYTRVLPDIKKSEKSKAFSTCGA 120

Db 160 LKNSGSDIKNELLLFLINGFNTLPVLAIVSYVIFCSILHKSRSKAFSTCGS 219

OY 121 HLFSVLYVGLPLFMVYVGPASGLAEDQDKVYSLFYTIIPFL 162

Db 220 HLMAVGIFGSIIFMYFKPSSNSLEQEKVSVYTVIIPML 261

RESULT 6

Q90807 PRELIMINARY; PRT; 312 AA.

AC Q90807; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

OS Olfactory Receptor 3 (FRAGMENT).

GN COR3.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

NCBI_TaxID=9031;

RM NCB1_TaxID=9031;

RP SEQUENCE FROM N.A.

RX MEDLINE-96184947; PubMed-8608858;

RA Lebowicz M., Lapointe F., Aletta P., Ayer-Le Lievre C.;

RT "Avian olfactory receptors: differentiation of olfactory neurons under normal and experimental conditions.";

RL Dev. Biol. 175:118-131(1996).

DR EMBL; X94743; CAA64369.1; -

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCR_RHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.

KW Receptor.

FT NON_TER

FT NON_TER

SO SEQUENCE 312 AA; 35258 MW; D629D3904184C098 CRC64;

Query Match 48.5%; Score 400; DB 13; Length 312;

Best Local Similarity 43.8%; Pred. No. 1.8e-33;

Matches 71; Conservative 47; Mismatches 44; Indels 0; Gaps 0;

OY 1 VAICNPPLLYVWMSNKLISAOQLSISYVIGFLHPLVHVSLLRLTFRCFNIIHYFCEIQ 60

Db 124 VAICRPLLYVWMSNKLISAOQLSISYVIGFLHPLVHVSLLRLTFRCFNIIHYFCEIQ 183

OY 61 LFKISCGPSINALIIFFGAFIQIPLMTIISYTRVLPDIKKSEKSKAFSTCGA 120

Db 184 LFOISSSTTLNELLYIFGSLFVWSSITITLISYVITITLVNIRSKDKYKAFSTCTS 243

OY 121 HLFSVLYVGLPLFMVYVGPASGLAEDQDKVYSLFYTIIPFL 162

Db 244 HLMAVSLFHGTIVIFMYVRSVKLSLDITDKIASLFTYTVIIPML 285

RESULT 7

Q9EOAO PRELIMINARY; PRT; 308 AA.

AC Q9EOAO; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RM NCB1_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=129/SVJ;

RX MEDLINE-21015403; PubMed-11130974;

RA Xie S.Y., Feinstein P., Mombaerts P.;

RT "Characterization of a cluster comprising 100 Odorant Receptor Genes in Mouse.";

RL Mamm. Genome 11:1070-1078(2000).

DR EMBL; AF282289; AAG39874.1; -

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCR_RHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.

KW Receptor.

SO SEQUENCE 308 AA; 34031 MW; 6279F1C7089AA820 CRC64;

Query Match 47.9%; Score 395; DB 11; Length 308;

Best Local Similarity 41.4%; Pred. No. 5.9e-33;

Matches 67; Conservative 46; Mismatches 49; Indels 0; Gaps 0;

OY 1 VAICNPPLLYVWMSNKLISAOQLSISYVIGFLHPLVHVSLLRLTFRCFNIIHYFCEIQ 60

Db 124 VAICRPLLYVWMSNKLISAOQLSISYVIGFLHPLVHVSLLRLTFRCFNIIHYFCEIQ 183

OY 61 LFKISCGPSINALIIFFGAFIQIPLMTIISYTRVLPDIKKSEKSKAFSTCGA 120

Db 184 LKNSGSDIKNELLLFLINGFNTLPVLAIVSYVIFCSILHKSRSKAFSTCGS 243

OY 121 HLFSVLYVGLPLFMVYVGPASGLAEDQDKVYSLFYTIIPFL 162

Db 244 HLMAVGIFGSIIFMYFKPSSNSLEQEKVSVYTVIIPML 285

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RESULT 8
0921V5 PRELIMINARY: PRT: 223 AA.
ID 0921V5
AC 0921V5
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE OLFACATORY RECEPTOR B3 (FRAGMENT).
GN OLF44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BL/6; TISSUE-OLFACATORY EPITHELIUM;
RX MEDLINE=99091050; PubMed=9875846;
RA Krautwurst D., Yau K.W., Reed R.R.;
RT "Identification of ligands for olfactory receptors by functional
RT expression of a receptor library.";
RL Cell 95:917-926(1998).
DR EMBL: AF102518; AAD13310.1; -
DR MGI: 1333829; Olf44.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 223 AA; 25089 MW; 83097D299076AF5E CRC64;

Query Match
Best Local Similarity 47.6%; Score 393; DB 11; Length 223;
Matches 70; Conservative 45; Mismatches 47; Indels 0; Gaps 0;

QY 1 VAICNPLPYVMMSNKLISQALSTISYVIGFLHPLVHVSLLRLTFCRFNIHYFCEIIQ 60
DB 61 VAICNPLNVMMSYQIYIFLISGVYIIGVICASANTGFWIRFCRLDIVINHYFCDLP 120
QY 61 LKRICNGPSINALIFIFGAFIQITLMTIITSYRVLFEDILKKSEGRSAFTSCGA 120
DB 121 LKLAOSNMYINMLIFGTINIFVPLITITISYIFIIASILIRISTEGRSKAFSTCS 180
QY 121 HLISVSLYGTLEFMYVRPASGLAEDQDVYSLEFYITIIPL 162
DB 181 HLAVAVFFGSLAFMYLQPSVSSMDQKVSSEFYITIVPML 222

RESULT 9
09EOB8 PRELIMINARY: PRT: 314 AA.
ID 09EOB8
AC 09EOB8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE ODORANT RECEPTOR K11.
GN ODO1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=21015403; PubMed=11130974;
RA Xie S.Y., Feinstein P., Mombaerts P.;
RT "Characterization of a Cluster Comprising 100 Odorant Receptor Genes
RT in Mouse.";
RL Mamm. Genome 11:1070-1078(2000).
DR EMBL: AF282271; AAG39856.1; -

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DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 314 AA; 35440 MW; 252457EBD336CE64 CRC64;

Query Match
Best Local Similarity 47.6%; Score 389; DB 11; Length 310;
Matches 78; Conservative 35; Mismatches 48; Indels 2; Gaps 2;

QY 1 VAICNPLPYVMMSNKLISQALSTISYVIGFLHPLVHVSLLRLTFCRFNIHYFCEIIQ 60
DB 123 VAICNPLNVMMSYQIYIFLISGVYIIGVICASANTGFWIRFCRLDIVINHYFCDLP 182
QY 61 LKRICNGPSINALIFIFGAFIQITLMTIITSYRVLFEDILKKSEGRSAFTSCG 119
DB 183 LKLAOSNMYINMLIFGTINIFVPLITITISYIFIIASILIRISTEGRSKAFSTCS 241
QY 120 HLISVSLYGTLEFMYVRPASGLAEDQDVYSLEFYITIIPL 162
DB 242 SHMIVLCLFFGSLAFMYLQPSVSLDQKVSSEFYITIVPML 284

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: June 27, 2002, 14:04:48 ; Search time 30.51 Seconds

(without alignments)
589.772 Million cell updates/sec

Title: US-09-747-155-225

Perfect score: 162

Sequence: 1 VAICNPPLYPMMSNKLSAQ.....LAEDQDKVSLFYITIIPLL 162

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq.032802.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	162	100.0	162	22	AAG98518	Human olfactory re
2	162	100.0	162	22	AAG72109	Human olfactory re
3	162	100.0	162	22	AAG72421.	Human OR-like poly
4	74	45.7	162	22	AAG98500	Pan troglodytes ol
5	18	11.1	314	22	AAU24633	Human olfactory re
6	18	11.1	314	22	AAG71500	Human olfactory re
7	18	11.1	314	22	AAG72474	Human OR-like poly
8	18	11.1	319	22	AAG71531	Human olfactory re
9	18	11.1	329	22	AAG71992	Human olfactory re
10	16	9.9	310	22	AAG71502	Human olfactory re
11	15	9.3	309	22	AAG71525	Human olfactory re

12	15	9.3	324	22	AAG71529	Human olfactory re
13	15	9.3	325	22	AAU24632	Human olfactory re
14	10	6.2	162	22	AAG98487	Papio hamdryas ol
15	10	6.2	162	22	AAU24584	Human olfactory re
16	10	6.2	312	22	AAG71635	Human olfactory re
17	10	6.2	316	22	AAE06769	Human G-protein co
18	10	6.2	316	22	AAG71567	Human olfactory re
19	10	6.2	316	22	AAG71946	Human olfactory re
20	10	6.2	328	22	AA66705	Human GPCR3 poly
21	10	6.2	333	22	AAG72658	Murine OR-like pol
22	10	6.2	333	22	AAG72682	Murine OR-like pol
23	9	5.6	124	22	AAAG9944	Human expressed po
24	9	5.6	124	22	AAAG9971	Human expressed po
25	9	5.6	124	22	ABH10248	Human cDNA seq ID
26	9	5.6	124	22	AAU18107	Novel human uterin
27	9	5.6	124	22	AAU18343	Human endocrine po
28	9	5.6	124	22	AAU18665	Renal and cardiova
29	9	5.6	124	22	AAAM89713	Human immune/haema
30	9	5.6	124	22	AAAG72165	Novel human neopla
31	9	5.6	125	22	AAAG72560	Human OR-like poly
32	9	5.6	157	22	AAAG71958	Human olfactory re
33	9	5.6	157	22	AAAG72041	Human olfactory re
34	9	5.6	159	22	AAAG72887	Human olfactory re
35	9	5.6	161	22	AAAG98574	Salimiri boliviensi
36	9	5.6	162	22	AAAG98488	Papio hamdryas ol
37	9	5.6	162	22	AAAG98516	Corilla olfactory
38	9	5.6	162	22	AAAG98528	Eulemar fulvus olf
39	9	5.6	162	22	AAAG98540	Maceca syriacus ol
40	9	5.6	162	22	AAAG98547	Callithrix jacchus
41	9	5.6	162	22	AAAG98550	Salimiri jacchus
42	9	5.6	162	22	AAAG98569	Salimiri seclureus o
43	9	5.6	162	22	AAAG98577	Salimiri boliviensi
44	9	5.6	162	22	AAAG72423	Human OR-like poly
45	9	5.6	179	22	AAAG72676	Murine OR-like poly

ALIGNMENTS

RESULT 1	
AAG98518	standard; Protein; 162 AA.
ID	
XX	
XX	AAAG98518:
XX	
XX	25-SEP-2001 (first entry)
XX	
DE	Human olfactory receptor 1.
XX	
KW	olfactory receptor; primate; mouse; human; food processing industry;
KW	aroma; perfume; toxic substance.
OS	
XX	Homo sapiens.
XX	
PN	WO200146262-A2.
XX	
PD	28-JUN-2001.
XX	
PF	22-DEC-2000; 2000WO-IB02017.
XX	
PR	22-DEC-1999; 99US-0171746.
XX	
PR	21-DEC-2000; 2000US-0747155.
XX	
PA	(CNRS) CNRS CENT NAT RECH SCI.
XX	
PI	Rouquier S, Giorgi D;
XX	
DR	WPI: 2001-381911/40.
XX	
DR	N-PSDB; AAH84009.
XX	
PT	Nucleic acids encoding primate and murine olfactory receptors, useful
XX	for analysis odours e.g. in food processing and perfume -

PS Claim 3; Page 266; 482pp; English.

CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours).

XX

SO Sequence 162 AA:

Query Match 100.0%; Score 162; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.9e-159;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAICNPILYPVWMSNKLISQOLISIVYGFELPHVNSLLRLTCRFRNIHYFCETIQ 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 valcnpilypvwmnsnklsqqlisysyvgflphlvnsllrltcrfnlhyfycellq 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 LFKISGNPSINALIIFFGAFIQIPTLMTIIISYTRVLFDLKKSEKGRSKAFSTCGA 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 lfkisgnpsinaliiffgafiqipltmtiisyrtrvlfdlkksekgrskafstcga 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 HLLSVSLYGYGTLIFWVVRPASGLAEDQDKVYSLFTTIIIPLL 162
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 hlsvsllygygtliffwvvrpasglaedqdkvyslfttllipll 162
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 2
 AAG72109
 ID AAG72109 standard; Protein: 162 AA.

XX AAG72109;
 AC
 XX 30-JUL-2001 (first entry)
 DT
 XX
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1790.
 XX
 KW Human: olfactory receptor; OR: primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation.
 XX
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US27582.
 XX
 PR 08-OCT-1999; 99US-0158615.
 XX
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX
 DR WPI: 2001-290713/30.
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 PS Claim 11; Page 1178; 1857pp; English.

CC The present sequence is an olfactory receptor which is encoded by
 CC one of a number of novel polynucleotides. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification
 CC of the odour receptors used to detect these primary scents. The methods
 CC also enable determination of secondary scents and the identification of

CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC faculties of different individuals.

XX

SO Sequence 162 AA:

Query Match 100.0%; Score 162; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.9e-159;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAICNPILYPVWMSNKLISQOLISIVYGFELPHVNSLLRLTCRFRNIHYFCETIQ 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 valcnpilypvwmnsnklsqqlisysyvgflphlvnsllrltcrfnlhyfycellq 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 LFKISGNPSINALIIFFGAFIQIPTLMTIIISYTRVLFDLKKSEKGRSKAFSTCGA 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 lfkisgnpsinaliiffgafiqipltmtiisyrtrvlfdlkksekgrskafstcga 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 HLLSVSLYGYGTLIFWVVRPASGLAEDQDKVYSLFTTIIIPLL 162
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 hlsvsllygygtliffwvvrpasglaedqdkvyslfttllipll 162
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3
 AAG72421
 ID AAG72421 standard; Protein: 162 AA.

XX AAG72421;
 AC
 XX 30-JUL-2001 (first entry)
 DT
 XX
 DE Human OR-like polypeptide query sequence, SEQ ID NO: 2102.
 XX
 KW Human: olfactory receptor; OR: primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation.
 XX
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US27582.
 XX
 PR 08-OCT-1999; 99US-0158615.
 XX
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX
 DR WPI: 2001-290713/30.
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 PS Example 6; Page 1411-1412; 1857pp; English.

CC The present sequence is a polypeptide encoded by one of 344 newly mined
 CC human genes. It was used as a query sequence in a database search of
 CC olfactory receptor (OR)-like sequences. The invention relates to isolated
 CC polynucleotides encoding polypeptides involved in olfactory sensation.
 CC The polynucleotides can be used in screening for olfactory agonists and
 CC antagonists. The methods allow for the determination of primary scents
 CC and the identification of the odour receptors used to detect these
 CC primary scents. The methods also enable determination of secondary scents

CC and the identification of combinations of odour receptors that are
 CC involved in detecting such secondary scents. This enables the
 CC construction of a scent representation (also called a scent fingerprint
 CC or scent profile), which may be used to re-create and edit scents.
 CC Libraries of olfactory receptors are useful for determining the
 CC interaction pattern of a composition with the receptors, and can be
 CC used for determining differences in the olfactory faculties of different
 CC individuals.
 CC
 XX Sequence 162 AA:

Query Match 100.0%; Score 162; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.9e-159;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAICNPDLVPVMSNKLSQLSISVIGFLHPLVHVSLLRLTFCRPNIIHYFCEIIQ 60
 DB 1 valcnpdlvpvmsnksqlsissyvlgflhplvhsllrltfcrfniihyfceilq 60
 QY 61 LFKISGNGPSINALLIFITGAFIQITLMTIIISTYRVLFEDILKKSEKSKAFSTCGA 120
 DB 61 lfkisngpsinalliffitgafiqitlmtiistyrvlfedilkksekyskafstcga 120
 QY 121 HLTSVSLYGTLLFMVVRPASGLAEDQDKVYSLEFYIIIPIL 162
 DB 121 hltsvsllygtllfmvvrpasglaedqdkvyslffyriiilpl 162

RESULT 4

AAG98500
 ID AAG98500 standard; Protein; 162 AA.

AC AAG98500;

DT 25-SEP-2001 (first entry)

DE Pan troglodytes olfactory receptor 9.

KW Olfactory receptor; primate; mouse; human; food processing industry;
 aromas; perfumery; toxic substance.

OS Pan troglodytes.

PN WO200146262-A2.

PD 28-JUN-2001.

PF 22-DEC-2000; 2000WO-1B02017.

PR 22-DEC-1999; 99US-0171746.

PR 21-DEC-2000; 2000US-0747155.

PA (CNRS) CNRS CENT NAT RECH SCI.

PI Rouquier S, Giorgi D;

DR WPI; 2001-381911/40.

DR N-PSDB; AAH83985.

PT Nucleic acids encoding primate and murine olfactory receptors, useful
 for analysis odours e.g. in food processing and perfumery -

PS Claim 3; Page 226; 482pp; English.

XX The invention relates to olfactory receptors (AAG98432-AAG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours).
 CC

SO Sequence 162 AA:

Query Match 45.7%; Score 74; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2.1e-68;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAICNPDLVPVMSNKLSQLSISVIGFLHPLVHVSLLRLTFCRPNIIHYFCEIIQ 60
 DB 1 valcnpdlvpvmsnksqlsissyvlgflhplvhsllrltfcrfniihyfceilq 60

QY 61 LFKISGNGPSINAL 74

DB 61 lfkisngpsinal 74

RESULT 5

AAU24633
 ID AAU24633 standard; Protein; 314 AA.

AC AAU24633;

DT 18-DEC-2001 (first entry)

DE Human olfactory receptor AOLFRL27.

KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 food additive; cosmetic; fragrance; pharmaceutical additive.

OS Homo sapiens.

PN WO200168805-A2.

PD 20-SEP-2001.

PF 13-MAR-2001; 2001WO-US07771.

PR 13-MAR-2000; 2000US-0188914.

PR 24-MAR-2000; 2000US-0192033.

PR 12-APR-2000; 2000US-0198474.

PR 24-APR-2000; 2000US-0199335.

PR 26-MAY-2000; 2000US-0207702.

PR 23-JUN-2000; 2000US-0213849.

PR 16-AUG-2000; 2000US-0226534.

PR 07-SEP-2000; 2000US-0230732.

PR 07-FEB-2001; 2001US-0266862.

PA (SENO-) SENOMYX INC.

PI Zozulya S;

DR WPI; 2001-570867/64.

DR N-PSDB; AAS42326.

PT Nucleic acids encoding human olfactory G protein-coupled receptors,
 useful for screening for compounds involved in olfactory sensation,
 where the compounds can be used in the food, pharmaceutical and
 cosmetic industries to customise odours -

PS Claim 60; Page 136; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence is a human olfactory receptor of the
 CC invention.
 CC

SO Sequence 314 AA:

Query Match 11.1%; Score 18; DB 22; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 KAFSTCGAHLISVSLYLG 130
|||||
DB 241 kafstcgahlisvsllyg 258

RESULT 6

AAG71500 ID AAG71500 standard; Protein: 314 AA.

XX AC AAG71500;

DT 30-JUL-2001 (first entry)

XX DE Human olfactory receptor polypeptide, SEQ ID NO: 1181.

XX KW Human; olfactory receptor; OR: primary scent determination;

KW secondary scent determination; polypeptide library; odour receptor;

XX KW scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

XX PN WO200127158-A2.

XX PD 19-APR-2001.

XX PF 06-OCT-2000; 2000WO-US27582.

XX PR 08-OCT-1999; 99US-0158615.

XX PR 24-FEB-2000; 2000US-0184809.

XX PA (DIGIT-) DIGISCENTS.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX DR WPI: 2001-290713/30.

XX PT New polynucleotides which encode polypeptides involved in olfactory

XX PS sensation for identifying olfactory agonists and antagonists -

XX PS Claim 11; Page 697-698; 1857pp; English.

XX CC The present sequence is an olfactory receptor which is encoded by

XX CC one of a number of novel polynucleotides. The polynucleotides can be

XX CC used in screening for olfactory agonists and antagonists. The methods

XX CC allow for the determination of primary scents and the identification

XX CC of the odour receptors used to detect these primary scents. The methods

XX CC also enable determination of secondary scents and the identification of

XX CC combinations of odour receptors that are involved in detecting such

XX CC secondary scents. This enables the construction of a scent representation

XX CC (also called a scent fingerprint or scent profile), which may be used to

XX CC re-create and edit scents. Libraries of olfactory receptors are useful

XX CC for determining the interaction pattern of a composition with the

XX CC receptors, and can be used for determining differences in the olfactory

XX CC faculties of different individuals.

XX SO Sequence 314 AA;

OY Query Match 11.1%; Score 18; DB 22; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 113 KAFSTCGAHLISVSLYLG 130
|||||
DB 241 kafstcgahlisvsllyg 258

RESULT 7

AAG72474 ID AAG72474 standard; Protein: 314 AA.

XX AC AAG72474;

DT 30-JUL-2001 (first entry)

XX DE Human OR-like polypeptide query sequence, SEQ ID NO: 2155.

XX KW Human; olfactory receptor; OR: primary scent determination;

KW secondary scent determination; polypeptide library; odour receptor;

XX KW scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

XX PN WO200127158-A2.

XX PD 19-APR-2001.

XX PF 06-OCT-2000; 2000WO-US27582.

XX PR 08-OCT-1999; 99US-0158615.

XX PR 24-FEB-2000; 2000US-0184809.

XX PA (DIGIT-) DIGISCENTS.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX DR WPI: 2001-290713/30.

XX PT New polynucleotides which encode polypeptides involved in olfactory

XX PS sensation for identifying olfactory agonists and antagonists -

XX PS Example 6; Page 1448-1449; 1857pp; English.

XX CC The present sequence is a polypeptide encoded by one of 344 newly mined

XX CC human genes. It was used as a query sequence in a database search of

XX CC olfactory receptor (OR)-like sequences. The invention relates to isolated

XX CC polynucleotides encoding polypeptides involved in olfactory sensation.

XX CC The polynucleotides can be used in screening for olfactory agonists and

XX CC antagonists. The methods allow for the determination of primary scents

XX CC and the identification of the odour receptors used to detect these

XX CC primary scents. The methods also enable determination of secondary scents

XX CC and the identification of combinations of odour receptors that are

XX CC involved in detecting such secondary scents. This enables the

XX CC construction of a scent representation (also called a scent fingerprint

XX CC or scent profile), which may be used to re-create and edit scents.

XX CC Libraries of olfactory receptors are useful for determining the

XX CC interaction pattern of a composition with the receptors, and can be

XX CC used for determining differences in the olfactory faculties of different

XX CC individuals.

XX SO Sequence 314 AA;

OY Query Match 11.1%; Score 18; DB 22; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 113 KAFSTCGAHLISVSLYLG 130
|||||
DB 241 kafstcgahlisvsllyg 258

RESULT 8

AAG71531 ID AAG71531 standard; Protein: 319 AA.

AC AAG71531;

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XX 31-JUL-2001 (first entry)
XX
XX
DE Human olfactory receptor polypeptide, SEQ ID NO: 1212.
XX
XX Human: olfactory receptor; OR: primary scent determination;
XX secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation.
OS Homo sapiens.
XX
XX WO200127158-A2.
XX
XX 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US27582.
XX
XX 08-OCT-1999; 99US-0158615.
XX 24-FEB-2000; 2000US-0184809.
XX
XX (DIGI-) DIGISCENTS.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
XX
XX New polynucleotides which encode polypeptides involved in olfactory
XX sensation for identifying olfactory agonists and antagonists -
XX
XX Claim 11: Page 722; 1857pp; English.
XX
XX The present sequence is an olfactory receptor which is encoded by
XX one of a number of novel polynucleotides. The polynucleotides can be
XX used in screening for olfactory agonists and antagonists. The methods
XX allow for the determination of primary scents and the identification
XX of the odour receptors used to detect these primary scents. The methods
XX also enable determination of secondary scents and the identification of
XX combinations of odour receptors that are involved in detecting such
XX secondary scents. This enables the construction of a scent representation
XX (also called a scent fingerprint or scent profile), which may be used to
XX re-create and edit scents. Libraries of olfactory receptors are useful
XX for determining the interaction pattern of a composition with the
XX receptors, and can be used for determining differences in the olfactory
XX faculties of different individuals.
XX
XX Sequence 319 AA;
SQ

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Query Match 11.1%; Score 18; DB 22; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 113 KAFSTCGAHLVSYSLYYG 130
   |||||||
Db 236 kstscgahlsvsllyyg 253

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RESULT 9
AAG71992
ID AAG71992 standard; Protein; 329 AA.
XX
XX AAG71992;
AC
XX
XX 31-JUL-2001 (first entry)
XX
XX Human olfactory receptor polypeptide, SEQ ID NO: 1673.
DE
XX
XX Human: olfactory receptor; OR: primary scent determination;
XX secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation.
XX
XX Homo sapiens.
OS

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XX
XX WO200127158-A2.
XX
XX 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US27582.
XX
XX 08-OCT-1999; 99US-0158615.
XX 24-FEB-2000; 2000US-0184809.
XX
XX (DIGI-) DIGISCENTS.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
XX
XX New polynucleotides which encode polypeptides involved in olfactory
XX sensation for identifying olfactory agonists and antagonists -
XX
XX Claim 11: Page 1092-1093; 1857pp; English.
XX
XX The present sequence is an olfactory receptor which is encoded by
XX one of a number of novel polynucleotides. The polynucleotides can be
XX used in screening for olfactory agonists and antagonists. The methods
XX allow for the determination of primary scents and the identification
XX of the odour receptors used to detect these primary scents. The methods
XX also enable determination of secondary scents and the identification of
XX combinations of odour receptors that are involved in detecting such
XX secondary scents. This enables the construction of a scent representation
XX (also called a scent fingerprint or scent profile), which may be used to
XX re-create and edit scents. Libraries of olfactory receptors are useful
XX for determining the interaction pattern of a composition with the
XX receptors, and can be used for determining differences in the olfactory
XX faculties of different individuals.
XX
XX Sequence 329 AA;
SQ

```

```

Query Match 11.1%; Score 18; DB 22; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 49 NIHFYCEIQLPKISC 66
   |||||||
Db 172 nihfyceiqlpkisc 189

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RESULT 10
AAG71502
ID AAG71502 standard; Protein; 310 AA.
XX
XX AAG71502;
AC
XX
XX 31-JUL-2001 (first entry)
XX
XX Human olfactory receptor polypeptide, SEQ ID NO: 1183.
DE
XX
XX Human: olfactory receptor; OR: primary scent determination;
XX secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation.
XX
XX Homo sapiens.
OS

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XX
XX WO200127158-A2.
XX
XX 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US27582.
XX
XX 08-OCT-1999; 99US-0158615.
XX 24-FEB-2000; 2000US-0184809.
XX

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PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI: 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PS sensation for identifying olfactory agonists and antagonists -
XX
PS Claim 11; Page 698-699; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals.
XX
SQ Sequence 310 AA;

Query Match 9.9%; Score 16; DB 22; Length 310;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 KAFSTCGAHLVSLSLY 128
|||
DB 231 kafstcgahllsvslly 246

RESULT 11
AAG71525
ID AAG71525 standard; Protein: 309 AA.
XX
AC AAG71525;
XX
DT 30-JUL-2001 (first entry)
XX
DE Human olfactory receptor polypeptide, SEQ ID NO: 1206.
XX
KM Human; olfactory receptor; OR; primary scent determination;
KM secondary scent determination; polypeptide library; odour receptor;
KM scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000MO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI: 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX

PS Claim 11; Page 717 and 684; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals.
XX
SQ Sequence 309 AA;

Query Match 9.3%; Score 15; DB 22; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 116 STCGAHLVSLSLYG 130
|||
DB 239 stcgahllsvsllyg 253

RESULT 12
AAG71529
ID AAG71529 standard; Protein: 324 AA.
XX
AC AAG71529;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human olfactory receptor polypeptide, SEQ ID NO: 1210.
XX
KM Human; olfactory receptor; OR; primary scent determination;
KM secondary scent determination; polypeptide library; odour receptor;
KM scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000MO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI: 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
PS Claim 11; Page 720-721; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation

CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC facilities of different individuals.

XX Sequence 324 AA;

Query Match 9.3%; Score 15; DB 22; Length 324;

Best Local Similarity 100.0%; Pred. No. 4.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 116 STCGAHLISVSLYYG 130
 |||||||
 DB 239 stcgaahlisvsllyg 253

RESULT 13

AAU24632
 ID AAU24632 standard; Protein; 325 AA.

XX AC AAU24632;

XX DF 18-DEC-2001 (first entry)

XX DE Human olfactory receptor AOLFRI26.

XX KM Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 food additive; cosmetic; fragrance; pharmaceutical additive.

XX OS Homo sapiens.

XX PN WO200168805-A2.

XX PD 20-SEP-2001.

XX PF 13-MAR-2001; 2001WO-US07771.

XX PR 13-MAR-2000; 2000US-0188914.

XX PR 24-MAR-2000; 2000US-0192033.

XX PR 12-APR-2000; 2000US-0198474.

XX PR 24-APR-2000; 2000US-0199335.

XX PR 26-MAY-2000; 2000US-0207702.

XX PR 23-JUN-2000; 2000US-0213849.

XX PR 16-AUG-2000; 2000US-0226534.

XX PR 07-SEP-2000; 2000US-0230732.

XX PR 07-FEB-2001; 2001US-0266862.

XX PA (SENO-) SENOMYX INC.

XX PI Zozulya S;

XX DR WPI; 2001-570867/64.

XX DR N-PSDB; AAS42325.

XX PT Nucleic acids encoding human olfactory G protein-coupled receptors,
 useful for screening for compounds involved in olfactory sensation,
 where the compounds can be used in the food, pharmaceutical and
 cosmetic industries to customise odours -

XX PT cosmetic industries to customise odours -

XX PS Claim 60; Page 136; 319pp; English.

XX CC The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence is a human olfactory receptor of the

CC invention.
 XX Sequence 325 AA;

Query Match 9.3%; Score 15; DB 22; Length 325;

Best Local Similarity 100.0%; Pred. No. 4.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 116 STCGAHLISVSLYYG 130
 |||||||
 DB 255 stcgaahlisvsllyg 269

RESULT 14.

AAU24584
 ID AAG98487 standard; Protein; 162 AA.

XX AC AAG98487;

XX DF 25-SEP-2001 (first entry)

XX DE Papio hamadryas olfactory receptor 12.

XX KM Olfactory receptor; primate; mouse; human; food processing industry;
 aromas; perfumery; toxic substance.

XX OS Papio hamadryas.

XX PN WO200146262-A2.

XX PD 28-JUN-2001.

XX PF 22-DEC-2000; 2000WO-IB02017.

XX PR 22-DEC-1999; 99US-0171746.

XX PR 21-DEC-2000; 2000US-0747155.

XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Rouquier S, Giorgi D;

XX DR WPI; 2001-381911/40.

XX DR N-PSDB; AAH83971.

XX PT Nucleic acids encoding primate and murine olfactory receptors, useful
 for analysis odours e.g. in food processing and perfumery -

XX PS Claim 3; Page 199; 482pp; English.

XX CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours).

XX SQ Sequence 162 AA;

Query Match 6.2%; Score 10; DB 22; Length 162;

Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 KAFSTCGAHL 122
 |||||||
 DB 113 kfstcgaahl 122

RESULT 15

AAU24584
 ID AAU24584 standard; Protein; 312 AA.

XX AAU24584;
AC 18-DEC-2001 (first entry)
XX
DT
XX
DE Human olfactory receptor AOLF74.
XX
XX Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
KM food additive; cosmetic; fragrance; pharmaceutical additive.
XX
OS Homo sapiens.
XX
PN WO200168805-A2.
XX
PD 20-SEP-2001.
XX
PE 13-MAR-2001; 2001WO-US07771.
XX
PR 13-MAR-2000; 2000US-0188914.
PR 24-MAR-2000; 2000US-0192033.
PR 12-APR-2000; 2000US-0198474.
PR 24-APR-2000; 2000US-0199335.
PR 26-MAY-2000; 2000US-0207702.
PR 23-JUN-2000; 2000US-0213849.
PR 16-AUG-2000; 2000US-0226534.
PR 07-SEP-2000; 2000US-0230732.
PR 07-FEB-2001; 2001US-0268662.
XX
PA (SENO-) SENOMYX INC.
XX
PI Zozulya S;
XX
DR N-PSDB; AAS42277.
XX
XX
PT Nucleic acids encoding human olfactory G protein-coupled receptors,
PT useful for screening for compounds involved in olfactory sensation,
PT where the compounds can be used in the food, pharmaceutical and
PT cosmetic industries to customise odours -
XX
XX
PS Claim 60; Page 114; 319pp; English.
XX
XX
CC The invention relates to nucleic acids encoding human olfactory
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
CC specifically recognise molecules, odourants, that elicit specific
CC olfactory sensation. The human olfactory receptors and polynucleotides
CC encoding them are useful for screening a library of chemical compounds
CC for compounds that are involved in olfactory sensation. Modulators of
CC their activity are useful for pharmacological and genetic modulation of
CC olfactory signalling pathways. Therefore, they can be used in the food,
CC pharmaceutical and cosmetic industries to customise odours and
CC fragrances. The present sequence is a human olfactory receptor of the
CC invention.
XX
XX
SQ Sequence 312 AA:

Query Match 6.2%; Score 10; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 KAFSTCGAHL 122
|||
Db 235 kafstcgahl 244

Search completed: June 27, 2002, 14:12:19
Job time: 451 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 14:08:18 ; Search time 15.87 seconds
(without alignments)
249.335 Million cell updates/sec

Title: US-09-747-155-225

Perfect score: 162

Sequence: 1 VAICNPILLYVMMSNKLDAQ.....LAEDQDKVYSIFITIIPL 162

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	4.3	247	1	US-08-465-980-3
2	7	4.3	247	2	US-09-053-303-3
3	7	4.3	247	5	PCT-US95-07093-3
4	7	4.3	284	1	US-08-118-270-67
5	7	4.3	284	5	PCT-US93-08528-67
6	7	4.3	314	3	US-08-988-876-7
7	7	4.3	504	2	US-08-466-589-4
8	7	4.3	504	2	US-08-700-636-4
9	7	4.3	504	3	US-08-467-574-4
10	7	4.3	504	4	US-09-217-345-4
11	7	4.3	541	4	US-09-158-767-19
12	7	4.3	541	4	US-09-158-767-20
13	7	4.3	584	1	US-08-448-196A-7
14	7	4.3	606	2	US-08-883-534-3
15	7	4.3	606	3	US-09-204-764-3
16	7	4.3	1302	1	US-08-232-537-2
17	7	4.3	4551	3	US-09-320-878-1
18	7	4.3	4613	4	US-09-105-537-31
19	7	4.3	5215	4	US-09-105-537-2
20	7	4.3	11877	4	US-09-105-537-6
21	6	3.7	13	4	US-09-461-697-15
22	6	3.7	16	1	US-08-196-630A-9
23	6	3.7	22	1	US-08-196-630A-8
24	6	3.7	37	2	US-08-942-423-5
25	6	3.7	43	2	US-08-389-360-2
26	6	3.7	43	3	US-09-038-328-2
27	6	3.7	67	2	US-08-639-857-31

28	6	3.7	70	1	US-08-466-033-185	Sequence 185, App
29	6	3.7	70	2	US-08-444-733-185	Sequence 185, App
30	6	3.7	70	2	US-08-464-134-185	Sequence 185, App
31	6	3.7	70	2	US-08-461-361-185	Sequence 185, App
32	6	3.7	70	2	US-08-485-910-185	Sequence 185, App
33	6	3.7	81	2	US-08-332-562A-86	Sequence 86, App1
34	6	3.7	96	1	US-08-488-113B-158	Sequence 158, App
35	6	3.7	96	1	US-08-477-484B-158	Sequence 158, App
36	6	3.7	96	1	US-08-107-669D-22	Sequence 22, App1
37	6	3.7	96	1	US-08-472-788A-22	Sequence 22, App1
38	6	3.7	96	2	US-08-477-531B-22	Sequence 22, App1
39	6	3.7	96	2	US-08-646-360-158	Sequence 158, App1
40	6	3.7	96	2	US-08-082-842A-22	Sequence 22, App1
41	6	3.7	96	4	US-08-839-765-158	Sequence 158, App
42	6	3.7	96	4	US-09-136-389-158	Sequence 158, App
43	6	3.7	131	1	US-08-466-033-179	Sequence 179, App
44	6	3.7	131	2	US-08-444-733-179	Sequence 179, App
45	6	3.7	131	2	US-08-464-134-179	Sequence 179, App

ALIGNMENTS

RESULT 1
US-08-465-980-3
; Sequence 3, Application US/08465980
; Patent No. 5756309
; GENERAL INFORMATION:
; APPLICANT: Soppel, Daniel R.
; APPLICANT: Li, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HRAU70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARRELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,980
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-980-3

Query Match 4.3%; Score 7; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 KARSTCG 119

Db 225 KAFSTCG 231

RESULT 2
US-09-053-303-3

; Sequence 3, Application US/09053303
; Patent No. 5948890
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: LI, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,303
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,980
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-053-303-3

Query Match 4.3%; Score 7; DB 2: Length 247;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 KAFSTCG 119
Db 225 KAFSTCG 231

RESULT 3
PCT-US95-07093-3
; Sequence 3, Application PC/TUS9507093
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: LI, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07093-3

Query Match 4.3%; Score 7; DB 5: Length 247;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 KAFSTCG 119
Db 225 KAFSTCG 231

RESULT 4
US-08-118-270-67
; Sequence 67, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-67

Query Match 4.3%; Score 7; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 KAFSTCG 119
Db 208 KAFSTCG 214

RESULT 5
PCT-US93-08528-67
Sequence 67, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-67

Query Match 4.3%; Score 7; DB 5; Length 284;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 KAFSTCG 119
Db 208 KAFSTCG 214

RESULT 6
US-08-988-876-7
Sequence 7, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ballings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 32086
US-08-988-876-7

Query Match 4.3%; Score 7; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 KAFSTCG 119
Db 236 KAFSTCG 242

RESULT 7
US-08-466-589-4
Sequence 4, Application US/08466589
Patent No. 5837489
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Ellis, Steven B.

APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
CLASSIFICATION: 536
FILING DATE: June 5, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9950
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-466-589-4

Query Match 4.3%; Score 7; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 SLEFYTHI 158
Db 240 SLEFYTHI 246

RESULT 8
US-08-700-636-4
Sequence 4, Application US/08700636
Patent No. 5910582
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,636
FILING DATE: 16-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-700-636-4

Query Match 4.3%; Score 7; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 SLEFYTHI 158
Db 240 SLEFYTHI 246

RESULT 9
US-08-467-574-4
Sequence 4, Application US/08467574
Patent No. 6022704
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 504 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-467-574-4

Query Match 4.3%; Score 7; DB 3; Length 504;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 152 SLFFYII 158
 |||||||
 DB 240 SLFFYII 246

RESULT 10
 US-09-217-345-4
 ; Sequence 4, Application US/09217345
 ; Patent No. 6303753
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Heller Ehrman White & McAuliffe
 ; STREET: 4250 Executive Square, 7th Floor
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/217,345
 ; FILING DATE: 21-DEC-98
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/467,574
 ; FILING DATE: 05-JUN-95
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/466,589,
 ; FILING DATE: 05-JUN-95
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-93
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 24735-9949B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-450-8400
 ; TELEFAX: 619-587-5360
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 504 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-09-217-345-4

Query Match 4.3%; Score 7; DB 4; Length 504;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 152 SLFFYII 158
 |||||||
 DB 240 SLFFYII 246

RESULT 11
 US-09-158-767-19
 ; Sequence 19, Application US/09158767A
 ; Patent No. 6180363
 ; GENERAL INFORMATION:
 ; APPLICANT: Batard, Yannick
 ; APPLICANT: Durst, Francis
 ; APPLICANT: Schalk, Michel
 ; APPLICANT: Werck-Reichardt, Daniele
 ; TITLE OF INVENTION: RECODING OF DNA SEQUENCES PERMITTING
 ; FILE REFERENCE: A32000
 ; CURRENT APPLICATION NUMBER: US/09/158,767A
 ; CURRENT FILING DATE: 1998-09-23
 ; EARLIER APPLICATION NUMBER: FR 97-12094
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 541
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Altered sequences
 ; US-09-158-767-19

Query Match 4.3%; Score 7; DB 4; Length 541;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 LLRLTF 45
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 DB 178 LLRLTF 184

RESULT 12
 US-09-158-767-20
 ; Sequence 20, Application US/09158767A
 ; Patent No. 6180363
 ; GENERAL INFORMATION:
 ; APPLICANT: Batard, Yannick
 ; APPLICANT: Durst, Francis
 ; APPLICANT: Schalk, Michel
 ; APPLICANT: Werck-Reichardt, Daniele
 ; TITLE OF INVENTION: RECODING OF DNA SEQUENCES PERMITTING
 ; FILE REFERENCE: A32000
 ; CURRENT APPLICATION NUMBER: US/09/158,767A
 ; CURRENT FILING DATE: 1998-09-23
 ; EARLIER APPLICATION NUMBER: FR 97-12094
 ; EARLIER FILING DATE: 1997-09-24
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 20
 ; LENGTH: 541
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Altered sequences
 ; US-09-158-767-20

Query Match 4.3%; Score 7; DB 4; Length 541;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 LLLRLTF 45
|111111|
Db 178 LLLRLTF 184

RESULT 13

US-08-448-196A-7
Sequence 7, Application US/08448196A
Patent No. 5780594
GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
TITLE OF INVENTION: RELATED PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NASA
STREET: MARSHALL SPACE FLIGHT CENTER
CITY: HUNTSVILLE
STATE: ALABAMA
COUNTRY: USA
ZIP: 35812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BROAD JR., ROBERT L.
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
TELEFAX: 205-544-0258
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-448-196A-7

Query Match 4.3%; Score 7; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 VSLLRL 43
|111111|
Db 343 VSLLRL 349

RESULT 14
US-08-883-534-3
Sequence 3, Application US/08883534
Patent No. 5846777
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,534
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0332 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: NEUTGMT01
CLONE: 1221143
US-08-883-534-3

Query Match 4.3%; Score 7; DB 2; Length 606;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 121 HLISVSL 127
|111111|
Db 291 HLISVSL 297

RESULT 15
US-09-204-764-3
Sequence 3, Application US/09204764
Patent No. 6025464
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/204,764
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/883,534
FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0332 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 606 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: NEUTGWT01
; CLONE: 1221143
; US-09-204-764-3

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Query Match          4.3%; Score 7; DB 3; Length 606;
Best Local Similarity 100.0%; Pred.No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 121 HLISVSL 127
   |||||
Db 291 HLISVSL 297

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Search completed: June 27, 2002, 14:12:56
Job time: 278 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 14:09:18 ; Search time 18.79 seconds

(without alignments)
828,444 Million cell updates/sec

Title: US-09-747-155-225

Perfect score: 162

Sequence: 1 VAICNPPLYPVMSNKLSAQ.....LAEDQDKVSLFTIIIPLL 162

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	5.6	157	2	S58038 Probable olfactory
2	9	5.6	157	2	S57998 Probable olfactory
3	9	5.6	157	2	S58017 Probable olfactory
4	9	5.6	157	2	S58014 Probable olfactory
5	9	5.6	157	2	S58007 Probable olfactory
6	9	5.6	222	2	C40745 odorant receptor (
7	9	5.6	304	2	S29709 olfactory receptor
8	8	4.9	136	2	PN0529 G protein-coupled
9	8	4.9	333	1	C69812 ferrichrome ABC tr
10	8	4.9	786	2	A69927 ribonucleoside-dip
11	8	4.9	1084	1	T12925 ribonucleotide red
12	7	4.3	81	2	W5WL35 E5 protein - human
13	7	4.3	132	2	D90362 hypothetical prote
14	7	4.3	135	2	PN0530 G protein-coupled
15	7	4.3	135	2	PN0527 G protein-coupled
16	7	4.3	147	2	T17958 hypothetical prote
17	7	4.3	157	2	S58031 Probable olfactory
18	7	4.3	157	2	S58004 Probable olfactory
19	7	4.3	157	2	S57995 Probable olfactory
20	7	4.3	157	2	S58001 Probable olfactory
21	7	4.3	157	2	S58013 Probable olfactory
22	7	4.3	157	2	S58067 Probable olfactory
23	7	4.3	157	2	S58030 Probable olfactory
24	7	4.3	157	2	S58018 Probable olfactory
25	7	4.3	157	2	S57996 Probable olfactory
26	7	4.3	185	2	S28996 G protein-coupled
27	7	4.3	204	2	AH2119 hypothetical prote
28	7	4.3	216	2	I38470 olfactory receptor
29	7	4.3	216	2	I38474 olfactory receptor

30	7	4.3	216	2	I38482 olfactory receptor
31	7	4.3	216	2	I38483 olfactory receptor
32	7	4.3	216	2	I38480 olfactory receptor
33	7	4.3	216	2	I38479 olfactory receptor
34	7	4.3	216	2	I38476 olfactory receptor
35	7	4.3	216	2	I38477 olfactory receptor
36	7	4.3	216	2	I38484 olfactory receptor
37	7	4.3	217	2	T28343 hypothetical prote
38	7	4.3	222	2	B40745 odorant receptor (
39	7	4.3	225	2	I38478 olfactory receptor
40	7	4.3	232	2	C72609 hypothetical prote
41	7	4.3	234	2	S28999 G protein-coupled
42	7	4.3	234	2	S28998 G protein-coupled
43	7	4.3	264	2	PC4369 olfactory receptor
44	7	4.3	265	2	I46986 albumin - dog (fra
45	7	4.3	275	2	S47325 myod protein - zeb

ALIGNMENTS

RESULT 1
S58038 Probable olfactory receptor tpcr21 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
R:Vanderhaeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
submitted to the EMBL Data Library, July 1995
A:Description: Male germ cells from several mammalian species express a specific repe
A:Reference number: S57995
A:Accession: S58038
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-157 <VAN>
A:Cross-references: EMBL:X89704; NID:g902724; PIDN:CAA61851.1; PID:g902725
C:Superfamily: olfactory receptor OR14

Query Match 5.6%; Score 9; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GRSKAFSTC 118
Db 108 GRSKAFSTC 116

RESULT 2
S57998 Probable olfactory receptor tpcr79 - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
R:Vanderhaeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
submitted to the EMBL Data Library, July 1995
A:Description: Male germ cells from several mammalian species express a specific repe
A:Reference number: S57995
A:Accession: S57998
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-157 <VAN>
A:Cross-references: EMBL:X89665; NID:g902198; PIDN:CAA61812.1; PID:g902199
C:Superfamily: olfactory receptor OR14

Query Match 5.6%; Score 9; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GRSKAFSTC 118
Db 108 GRSKAFSTC 116

RESULT 3
S58017
Probable olfactory receptor tpcr25 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
C:Accession: S58017
R:Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentlier, M.
submitted to the EMBL Data Library, July 1995
A:Description: Male germ cells from several mammalian species express a specific repertoire
A:Reference number: S57995
A:Accession: S58017
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-157 <VAN>
A:Cross-references: EMBL:X89672; NID:g902327; PIDN:CAA61819.1; PID:g902328
C:Superfamily: olfactory receptor OR14

Query Match 5.6%; Score 9; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTC 118
|||||
Db 108 GRSKAFSTC 116

RESULT 4
S58014
Probable olfactory receptor tpcr120 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
C:Accession: S58014
R:Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentlier, M.
submitted to the EMBL Data Library, July 1995
A:Description: Male germ cells from several mammalian species express a specific repertoire
A:Reference number: S57995
A:Accession: S58014
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-157 <VAN>
A:Cross-references: EMBL:X89669; NID:g902321; PIDN:CAA61816.1; PID:g902322
C:Superfamily: olfactory receptor OR14

Query Match 5.6%; Score 9; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTC 118
|||||
Db 108 GRSKAFSTC 116

RESULT 5
S58007
Probable olfactory receptor tpcr85 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 26-Aug-1999
C:Accession: S58007
R:Vanderhaeghen, P.; Schurmans, S.; Vassart, G.; Parmentlier, M.
submitted to the EMBL Data Library, July 1995
A:Description: Male germ cells from several mammalian species express a specific repertoire
A:Reference number: S57995
A:Accession: S58007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-157 <VAN>
A:Cross-references: EMBL:X89675; NID:g902333; PIDN:CAA61822.1; PID:g902334
C:Superfamily: olfactory receptor OR14

Query Match 5.6%; Score 9; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTC 118
|||||
Db 108 GRSKAFSTC 116

RESULT 6
C40745
Odorant receptor (clone K7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C:Accession: C40745
R:Bessler, K.J.; Sullivan, S.L.; Buck, L.B.
Cell 73, 597-609, 1993
A:Title: A zonal organization of odorant receptor gene expression in the olfactory epithelium
A:Reference number: M40745; MUID:93258822
A:Accession: C40745
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-222 <RES>
A:Cross-references: GB:L14569; NID:g293759; PIDN:AAA39853.1; PID:g293760
A:Experimental source: olfactory epithelium
A:Note: sequence extracted from NCBI backbone (NCBIP:131750)
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 5.6%; Score 9; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPILY 9
|||||
Db 64 VAICNPILY 72

RESULT 7
S29709
Olfactory receptor OR14 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C:Accession: S29709
R:Ramling, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Br
Nature 361, 353-356, 1993
A:Title: Cloning and expression of odorant receptors.
A:Reference number: S29707; MUID:93149273
A:Accession: S29709
A:Molecule type: mRNA
A:Residues: 1-304 <RAW>
C:Superfamily: olfactory receptor OR14

Query Match 5.6%; Score 9; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTC 118
|||||
Db 226 GRSKAFSTC 234

RESULT 8
PN0529
G protein-coupled receptor type A (clone TAS 7) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 03-Nov-2000
C:Accession: PN0529
R:Matsuka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A>Title: Identification of novel members of G-protein coupled receptor superfamily expre
 A:Reference number: JN0621; MID:93326166
 A:Accession: PN0529
 A:Molecule type: mRNA
 A:Residues: 1-136 <MAT>
 A:Experimental source: tongue taste papillae
 C:Comment: This protein is involved in modulating taste sensitivity or regeneration of t
 C:Superfamily: olfactory receptor OR14
 C:Keywords: receptor; transmembrane protein
 F:1-8/Domain: transmembrane #status predicted <TM1>
 F:28-46/Domain: transmembrane #status predicted <TM2>
 F:90-106/Domain: transmembrane #status predicted <TM3>
 F:125-135/Domain: transmembrane #status predicted <TM4>

Query Match 4.9%; Score 8; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AICNPPLY 9
 Db 13 AICNPPLY 20

RESULT 9
 C69812
 ferrichrome ABC transporter (permease) homolog yfmd - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: C69812
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertea
 A: Bron, S.; Brouillette, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gallie
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, X.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MID:98044033
 A:Accession: C69812
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-333 <KUN>
 A:Cross-references: GB:299108; GB:AL009126; NID:g2633055; PIDN:CAB12580.1; PID:g2633075
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yfmd
 C:Superfamily: ferrichrome ABC transporter

Query Match 4.9%; Score 8; DB 1; Length 333;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 ALIIFFG 80
 Db 19 ALIIFFG 26

RESULT 10
 A69927
 ribonucleoside-diphosphate reductase (alph) homolog yoso - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 03-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
 C:Accession: A69927
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertea

C.; Bron, S.; Brouillette, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gal
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, X.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MID:98044033
 A:Accession: A69927
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-786 <KUN>
 A:Cross-references: GB:299114; GB:AL009126; NID:g2634230; PIDN:CAB13897.1; PID:el1854
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yoso

Query Match 4.9%; Score 8; DB 2; Length 786;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 98 VLFIDILK 105
 Db 279 VLFIDILK 286

RESULT 11
 T12925
 ribonucleotide reductase large chain - Bacillus subtilis phage SPBc2
 C:Species: Bacillus subtilis phage SPBc2
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 02-Jun-2000
 C:Accession: T12925
 R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
 Submitted to the EMBL Data Library, August 1997
 A:Description: The complete nucleotide sequence of the Bacillus subtilis spbetac2 pro
 A:Reference number: 217583
 A:Accession: T12925
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1084 <LAZ>
 A:Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025639; PIDN:AC13134.1
 C:Genetics:
 A:Gene: bmrde

Query Match 4.9%; Score 8; DB 2; Length 1084;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 98 VLFIDILK 105
 Db 577 VLFIDILK 584

RESULT 12
 W5WL35
 E5 protein - human papillomavirus type 35
 C:Species: human papillomavirus type 35
 A:Note: host Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
 C:Accession: D40824
 R:Marich, J.E.; Ponsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
 Virology 186, 770-776, 1992
 A>Title: The phylogenetic relationship and complete nucleotide sequence of human papil
 A:Reference number: A40824; MID:92124753

A:Accession: D40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-81 <MAR>
A:Cross-references: GB:M74117; NID:q3333050; PIDN:AAA46970.1; PID:q3333056
C:Superfamily: papillomavirus E5 protein
C:Keywords: early protein

Query Match 4.3%; Score 7; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 122 LLSVSLY 128
|||||||
Db 32 LLSVSLY 38

RESULT 13
D90362
hypothetical protein SSO1964 [imported] - Sulfolobus solfataricus transposon ISC1913
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: D90362
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awaizer, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90362
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <KIR>
A:Cross-references: GB:AE006641; NID:q13815239; PIDN:AAK42155.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1964

Query Match 4.3%; Score 7; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 QLSISY 26
|||||||
Db 12 QLSISY 18

RESULT 14
PN0530
G:Protein-coupled receptor type A (clone TAS 38) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
C:Accession: PN0530
R:Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A:Title: Identification of novel members of G-protein coupled receptor superfamily ex-
A:Reference number: JN0621; MUID:93326166
A:Accession: PN0530
A:Molecule type: mRNA
A:Residues: 1-135 <MAT>
A:Experimental source: tongue taste papillae
C:Comment: This protein is involved in modulating taste sensitivity or regeneration of
C:Superfamily: olfactory receptor OR14
C:Keywords: receptor; transmembrane protein
F:1-8/Domain: transmembrane #status predicted <TM1>
F:28-46/Domain: transmembrane #status predicted <TM2>
F:91-106/Domain: transmembrane #status predicted <TM3>
F:125-135/Domain: transmembrane #status predicted <TM4>

Query Match 4.3%; Score 7; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VAICNPL 7
|||||||
Db 12 VAICNPL 18

RESULT 15
PN0527
G:Protein-coupled receptor type A (clone TAS 4) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 03-Nov-2000
C:Accession: PN0527
R:Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A:Title: Identification of novel members of G-protein coupled receptor superfamily ex
A:Reference number: JN0621; MUID:93326166
A:Accession: PN0527
A:Molecule type: DNA
A:Residues: 1-135 <MAT>
A:Experimental source: tongue taste papillae
A:Note: cross-reference
C:Comment: This protein is involved in modulating taste sensitivity or regeneration o
C:Superfamily: olfactory receptor OR14
C:Keywords: receptor; transmembrane protein
F:1-8/Domain: transmembrane #status predicted <TM1>
F:28-46/Domain: transmembrane #status predicted <TM2>
F:90-106/Domain: transmembrane #status predicted <TM3>
F:125-135/Domain: transmembrane #status predicted <TM4>

Query Match 4.3%; Score 7; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 KAFSTCG 119
|||||||
Db 124 KAFSTCG 130

Search completed: June 27, 2002, 14:13:35
Job time: 257 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2002, 14:12:58 ; Search time 10.69 Seconds
(without alignments)
586.770 Million cell updates/sec

Title: US-09-747-155-225

Perfect score: 162
Sequence: 1 VAICNPPLYVPMNSNKLAAQ.....LAEDQKVSLSFTITIIPL 162

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	5.6	159	1	OLFB_CHICK
2	9	5.6	222	1	OL7B_MOUSE
3	9	5.6	311	1	OL7B_MOUSE
4	9	5.6	311	1	OL7B_MOUSE
5	9	5.6	314	1	OL7B_MOUSE
6	9	5.6	314	1	OL7B_MOUSE
7	9	5.6	314	1	OL7B_MOUSE
8	9	5.6	314	1	OL7B_MOUSE
9	9	5.6	314	1	OL7B_MOUSE
10	9	5.6	314	1	OL7B_MOUSE
11	9	5.6	314	1	OL7B_MOUSE
12	9	5.6	314	1	OL7B_MOUSE
13	9	5.6	314	1	OL7B_MOUSE
14	9	5.6	314	1	OL7B_MOUSE
15	9	5.6	314	1	OL7B_MOUSE
16	9	5.6	314	1	OL7B_MOUSE
17	9	5.6	314	1	OL7B_MOUSE
18	9	5.6	314	1	OL7B_MOUSE
19	9	5.6	314	1	OL7B_MOUSE
20	9	5.6	314	1	OL7B_MOUSE
21	9	5.6	314	1	OL7B_MOUSE
22	9	5.6	314	1	OL7B_MOUSE
23	9	5.6	314	1	OL7B_MOUSE
24	9	5.6	314	1	OL7B_MOUSE
25	9	5.6	314	1	OL7B_MOUSE
26	9	5.6	314	1	OL7B_MOUSE
27	9	5.6	314	1	OL7B_MOUSE
28	9	5.6	314	1	OL7B_MOUSE
29	9	5.6	314	1	OL7B_MOUSE
30	9	5.6	314	1	OL7B_MOUSE
31	9	5.6	314	1	OL7B_MOUSE
32	9	5.6	314	1	OL7B_MOUSE
33	9	5.6	314	1	OL7B_MOUSE

34	7	4.3	320	1	OL7B_MOUSE
35	7	4.3	323	1	OL7B_MOUSE
36	7	4.3	330	1	OL7B_MOUSE
37	7	4.3	335	1	OL7B_MOUSE
38	7	4.3	355	1	OL7B_MOUSE
39	7	4.3	492	1	OL7B_MOUSE
40	7	4.3	492	1	OL7B_MOUSE
41	7	4.3	606	1	OL7B_MOUSE
42	7	4.3	608	1	OL7B_MOUSE
43	7	4.3	608	1	OL7B_MOUSE
44	7	4.3	608	1	OL7B_MOUSE
45	7	4.3	609	1	OL7B_MOUSE

ALIGNMENTS

RESULT	ID	STANDARD	PRT	159 AA
1	OLFB_CHICK			
AC	098913			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DE	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Olfactory receptor-like protein COR8 (Fragment).			
GN	COR8			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Olfactory epithelium;			
RX	MEDLINE=96317247; PubMed=8734500;			
RA	Nef S., Allaman I., Fiumelli H., de Castro E., Nef P.;			
RT	"Olfaction in birds: differential embryonic expression of nine			
RT	putative odorant receptor genes in the avian olfactory system.";			
RL	Mech. Dev. 55:65-77(1996).			
CC	-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation-			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL: 279591; CAB01852.1; -			
DR	GCRDB: GCR_1091;			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam: PF00001; 7tm.1; 1.			
DR	PROSITE: PS00237; G_PROTEIN_RECP_FL_1; PARTIAL.			
DR	PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Olfaction; Multigene family.			
FT	NON_TER	1		
FT	DOMAIN	<1	16	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	17	41	4 (POTENTIAL).
FT	DOMAIN	42	82	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	83	103	5 (POTENTIAL).
FT	DOMAIN	104	116	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	117	137	6 (POTENTIAL).
FT	DOMAIN	138	148	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	149	>159	7 (POTENTIAL).
FT	NON_TER	159	159	
SQ	SEQUENCE	159 AA; 17385 MW; B185619981A8B4E4 CRC64;		

Query Match

5.6%; Score 9; DB 1; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPPLY 9
Db 1 VAICNPPLY 9

```
RESULT 2
OL7B_MOUSE STANDARD; PRT; 222 AA.
AC P34983;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE Olfactory receptor 7B (K4) (Fragment).
GN OLF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=93258822; PubMed=7683976;
RA Reesler K.J., Sullivan S.L., Buck L.B.;
RT "A zonal organization of odorant receptor gene expression in the
RT olfactory epithelium";
RL Cell 73:597-609(1993).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: OLFACTORY RECEPTORS 7A-7I ARE PRODUCED BY EIGHT
CC DIFFERENT GENES WITHIN THE OLF7 COMPLEX.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; L14569; AAA39853.1; -
DR PIR; C40745; C40745.
DR GCRDB; GCR 0716; -
DR MGD; MGI:104712; Olf7.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
KW Olfaction.
FT NON_TER 1 1
FT TRANSMEM <1 19 2 (POTENTIAL).
FT DOMAIN 20 40 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 41 60 3 (POTENTIAL).
FT DOMAIN 61 79 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 98 4 (POTENTIAL).
FT DOMAIN 99 136 5 (POTENTIAL).
FT TRANSMEM 137 159 5 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 160 176 5 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 177 200 6 (POTENTIAL).
FT DOMAIN 201 212 6 (POTENTIAL).
FT TRANSMEM 213 >222. EXTRACELLULAR (POTENTIAL).
FT NON_TER 222 222 7 (POTENTIAL).
SQ SEQUENCE 222 AA; 24855 MW; 5C1978B5C93FC3E1 CRC64;
```

Query Match 5.6%; Score 9; DB 1; Length 222;

Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPPLY 9
Db 64 VAICNPPLY 72

```
RESULT 3
O8B8_HUMAN STANDARD; PRT; 311 AA.
ID O8B8_HUMAN
AC O15620;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 8B8 (Olfactory receptor TRCR85).
GN O8B8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE OF 126-282 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97224452; PubMed=9119360;
RA Vanderhaeghen P., Schurmann S., Vassart G., Parmentier M.;
RT "Specific repertoire of olfactory receptor genes in the male germ
RT cells of several mammalian species.";
RL Genomics 39:239-246(1997).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; X89675; CAA61822.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 50 57 2 (POTENTIAL).
FT TRANSMEM 58 79 2 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 80 100 3 (POTENTIAL).
FT TRANSMEM 101 120 3 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 121 139 4 (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 5 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 236 6 (POTENTIAL).
FT TRANSMEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 272 7 (POTENTIAL).
FT TRANSMEM 273 292 7 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 293 311 7 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 311 311 7 BY SIMILARITY.
FT DISULFID 97 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 5 5 G -> S (IN REF. 1).
FT CONFLICT 204 204
SQ SEQUENCE 311 AA; 34482 MW; 9D8AAC4DA179ABE5 CRC64;
```

Query Match 5.6%; Score 9; DB 1; Length 311;

Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPPLY 9
Db 1 VAICNPPLY 9

DB 124 VAICNPPLY 132

RESULT 4

OLFL_CANFA STANDARD; PRT; 311 AA.

ID OLFL_CANFA

AC Q95154;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Olfactory receptor-like protein OLFL.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97008103; PubMed=8855279;

RA Issel-Tarver L., Rine J.;

RT "Organization and expression of canine olfactory receptor genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:10897-10902(1996).

CC -1- FUNCTION: PUTATIVE ODORANT OR SPERM CELL RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: U53679; AAB37239.1; -

DR GCRDB; GCR_1192; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00245; OLFACTOR.

DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.

DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 24

FT TRANSMEM 25 48

FT DOMAIN 49 56

FT TRANSMEM 57 78

FT DOMAIN 79 99

FT TRANSMEM 100 119

FT DOMAIN 120 138

FT TRANSMEM 139 157

FT DOMAIN 158 195

FT TRANSMEM 196 218

FT DOMAIN 219 235

FT TRANSMEM 236 259

FT DOMAIN 260 271

FT TRANSMEM 272 291

FT DOMAIN 292 311

FT CARBOHD 311 4

SO SEQUENCE 311 AA; 35209 MW; 05A2132474F543A1 CRC64;

Query Match 5.6%; Score 9; DB 1; Length 311;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPPLY 9

ID 123 VAICNPPLY 131

RESULT 5

OSIL_HUMAN STANDARD; PRT; 314 AA.

AC Q13606;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Olfactory receptor 511 (Olfactory receptor-like protein OLFL).

GN OR511 OR OLFL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Issel-Tarver L., Rine J.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBS databases.

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: U56420; AAB01214.1; -

DR GCRDB; GCR_1925; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00245; OLFACTOR.

DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.

DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 28

FT TRANSMEM 29 51

FT DOMAIN 52 59

FT TRANSMEM 60 81

FT DOMAIN 82 102

FT TRANSMEM 103 122

FT DOMAIN 123 141

FT TRANSMEM 142 166

FT DOMAIN 167 207

FT TRANSMEM 208 228

FT DOMAIN 229 241

FT TRANSMEM 242 262

FT DOMAIN 263 273

FT TRANSMEM 274 294

FT DISULFD 295 314

FT CARBOHD 314 7

SO SEQUENCE 314 AA; 36048 MW; 334BE9BF39A4D63 CRC64;

Query Match 5.6%; Score 9; DB 1; Length 314;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPPLY 9

ID 126 VAICNPPLY 134

RESULT 6

VE5_HPV35 STANDARD; PRT; 81 AA.

ID VE5_HPV35

AC P27226;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Probable E5 protein.

GN E5.

OS Human Papillomavirus type 35.
CC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC Papillomavirus.
OX NCBI_TaxID=10587;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124753; PubMed=1310198;
RA Marich J.E., Porttler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
RT "The phylogenetic relationship and complete nucleotide sequence of
human papillomavirus type 35."
RL Virology 186:770-776(1992).
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CC -----
DR EMBL: M74117; AAA46970.1; -.
DR PIR: D40824; W5WLC35.
DR InterPro: IPR004270: Papilloma_E5.
DR Pfam: PF03025; Papilloma_E5; 1.
KW Early protein.
SQ SEQUENCE 81 AA; 9000 MW; B12A23102E72163B CRC64;

Query Match 4.3%; Score 7; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 LLSVSLY 128
|||
Db 32 LLSVSLY 38

RESULT 7
OL7H_MOUSE STANDARD; PRT; 111 AA.
ID OL7H_MOUSE
AC Q60893;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Olfactory receptor 7H (M71) (Fragment).
GN OLFR7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J;
RX MEDLINE=96149403; PubMed=8570653;
RA Sullivan S.L., Adamson M.C., Ressler K.J., Kozak C.A., Buck L.B.;
RT "The chromosomal distribution of mouse odorant receptor genes."
RL Proc. Natl. Acad. Sci. U.S.A. 93:884-888(1996).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: OLFACTORY RECEPTORS 7A-7I ARE PRODUCED BY EIGHT
CC DIFFERENT GENES WITHIN THE OLFR7 COMPLEX.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: U28782; AAC52405.1; -.
DR GCRDb: GCR_1678; -.

DR MGD: MGI:104712; Olfr7.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; PARTIAL.
DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
FT Olfaction.
FT NON_TER 1 1
FT DOMAIN <1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 33 4 (POTENTIAL).
FT DOMAIN 34 72 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 73 94 5 (POTENTIAL).
FT DOMAIN 95 108 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 109 >111 6 (POTENTIAL).
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12118 MW; 64D3ADFD4BB877D3 CRC64;

Query Match 4.3%; Score 7; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 GRSKAFS 116
|||
Db 105 GRSKAFS 111

RESULT 8
OL7C_MOUSE STANDARD; PRT; 112 AA.
ID OL7C_MOUSE
AC Q60882;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Olfactory receptor 7C (K21) (Fragment).
GN OLFR7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J;
RX MEDLINE=96149403; PubMed=8570653;
RA Sullivan S.L., Adamson M.C., Ressler K.J., Kozak C.A., Buck L.B.;
RT "The chromosomal distribution of mouse odorant receptor genes."
RL Proc. Natl. Acad. Sci. U.S.A. 93:884-888(1996).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: OLFACTORY RECEPTORS 7A-7I ARE PRODUCED BY EIGHT
CC DIFFERENT GENES WITHIN THE OLFR7 COMPLEX.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: U28771; AAC52394.1; -.
DR GCRDb: GCR_1690; -.
DR MGD: MGI:104712; Olfr7.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; PARTIAL.
DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Multigene family;
FT Olfaction.
FT NON_TER 1 1
FT DOMAIN <1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 33 4 (POTENTIAL).
FT TRANSMEM 34 72 5 (POTENTIAL).

FT DOMAIN 34 73 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 74 95 5 (POTENTIAL).
 FT DOMAIN 96 109 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 110 >112 6 (POTENTIAL).
 FT NON_TER 112 112
 SO SEQUENCE 112 AA; 12261 MW; BC1AD5ABBA6C78BB CRC64;

Query Match 4.3%; Score 7; DB 1; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFS 116
 |||||
 DB 106 GRSKAFS 112

RESULT 9
 OL7D_MOUSE STANDARD; PRT; 112 AA.
 AC 060884;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Olfactory receptor 7D (M15) (Fragment).
 GN OLFR7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=96149403; PubMed=6570653;
 RA Sullivan S.L., Adamson M.C., Ressler K.J., Kozak C.A., Buck L.B.;
 RT "The chromosomal distribution of mouse odorant receptor genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:884-888(1996).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- MISCELLANEOUS: OLFACTORY RECEPTORS 7A-7I ARE PRODUCED BY EIGHT
 CC DIFFERENT GENES WITHIN THE OLFR7 COMPLEX.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; U28773; AAC52396.1; -.
 DR GCRDB; GCR1688; -.
 DR MGD; MGI:104712; Olfr7.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_FL_1; PARTIAL.
 DR PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Multigene family;
 KW Olfaction.
 FT NON_TER 1 1
 FT DOMAIN <1 12 1 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 13 33 4 (POTENTIAL).
 FT DOMAIN 34 73 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 74 95 5 (POTENTIAL).
 FT DOMAIN 96 109 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 110 >112 6 (POTENTIAL).
 FT NON_TER 112 112
 SO SEQUENCE 112 AA; 12426 MW; 08640539B168518E CRC64;

Query Match 4.3%; Score 7; DB 1; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFS 116
 |||||
 DB 106 GRSKAFS 112

RESULT 10
 GU01_RAT STANDARD; PRT; 185 AA.
 ID GU01_RAT
 AC P35894;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Possible gustatory receptor clone PTE01 (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FISCHER; TISSUE=Lingual epithelium;
 RX MEDLINE=93138133; PubMed=8380780;
 RA Abe K., Kusakabe Y., Tanemura K., Emori Y., Arai S.;
 RT "Multiple genes for G protein-coupled receptors and their expression
 RT in lingual epithelia.";
 RL FEBS Lett. 316:253-256(1993).
 CC -1- FUNCTION: POSSIBLE TASTE RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: TONGUE-SPECIFIC.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC PIR: S28996; S28996.
 DR GCRDB; GCR0825; -.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_FL_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT NON_TER 1 1
 FT TRANSMEM <1 11 2 (POTENTIAL).
 FT DOMAIN 12 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 43 62 3 (POTENTIAL).
 FT DOMAIN 63 84 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 105 4 (POTENTIAL).
 FT DOMAIN 106 138 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 139 160 5 (POTENTIAL).
 FT DOMAIN 161 182 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 183 >185 6 (POTENTIAL).
 FT NON_TER 185 185
 SO SEQUENCE 185 AA; 20605 MW; FCF72E763D578F23 CRC64;

Query Match 4.3%; Score 7; DB 1; Length 185;
 Best Local Similarity 100.0%; Pred. No. 8.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 KAFSTCG 119
 |||||
 DB 178 KAFSTCG 184

RESULT 11
 O1E5_HUMAN STANDARD; PRT; 216 AA.
 ID O1E5_HUMAN
 AC Q9JUM60;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 1E5 (Olfactory receptor 13-66) (OR13-66)
 DE (Fragment).
 DE ORIES.
 OS Homo sapiens (Human).
 GN
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP MEDLINE=98160182; PubMed=9500546;
 RA Roudaut S., Tavian S., Trask B.J., Brand-Arpon V., van den Engh G.,
 RA Demallie J.G., Giorgi D.;
 RL "Distribution of Olfactory receptor genes in the human genome.";
 RL Nat. Genet. 18:243-250(1998).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: U06222; AAC39613.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT NON_TER 1
 FT TRANSSEM 1
 FT TRANSSEM <1 12 2 (POTENTIAL).
 FT DOMAIN 13 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 34 53 3 (POTENTIAL).
 FT DOMAIN 54 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 73 91 4 (POTENTIAL).
 FT DOMAIN 92 129 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 130 152 5 (POTENTIAL).
 FT DOMAIN 153 169 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 170 192 6 (POTENTIAL).
 FT DOMAIN 193 204 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 206 >216 7 (POTENTIAL).
 FT NON_TER 216
 SQ SEQUENCE 216 AA; 23977 MW; 0A48A7D1A98C244 CRC64;
 Query Match 4.3%; Score 7; DB 1; Length 216;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 113 KAFSTCG 119
 Db 169 KAFSTCG 175
 RESULT 12
 OLIF_HUMAN STANDARD; PRT; 216 AA.
 AC P47886;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor-like protein OR17-82 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota: Metazoa: Chordata: Craniala: Vertebrata: Euteleostomi;
 OC Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94272458; PubMed=8004088;
 RA Ben-Arie N., Lancel D., Taylor C., Khen M., Walker N.,
 RA Ledbetter D.H., Carrozzo R., Patel K., Sheer D., Lehrach H.,
 RA North M.A.;
 RT "Olfactory receptor gene cluster on human chromosome 17: possible
 RT duplication of an ancestral receptor repertoire.",
 CC

RL Hum. Mol. Genet. 3:229-235(1994).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: U04684; AAA18348.1; -
 DR GCRD: GCR_0851; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT NON_TER 1
 FT TRANSSEM 1
 FT TRANSSEM <1 12 2 (POTENTIAL).
 FT DOMAIN 13 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 34 53 3 (POTENTIAL).
 FT DOMAIN 54 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 74 91 4 (POTENTIAL).
 FT DOMAIN 92 129 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 130 153 5 (POTENTIAL).
 FT DOMAIN 154 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 171 194 6 (POTENTIAL).
 FT DOMAIN 195 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 206 >216 7 (POTENTIAL).
 FT NON_TER 216
 SQ SEQUENCE 216 AA; 23634 MW; ACC757FB3D9B55F CRC64;
 Query Match 4.3%; Score 7; DB 1; Length 216;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 113 KAFSTCG 119
 Db 169 KAFSTCG 175
 RESULT 13
 OLIF_HUMAN STANDARD; PRT; 216 AA.
 AC P47889;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor-like protein OR17-207 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota: Metazoa: Chordata: Craniala: Vertebrata: Euteleostomi;
 OC Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94272458; PubMed=8004088;
 RA Ben-Arie N., Lancel D., Taylor C., Khen M., Walker N.,
 RA Ledbetter D.H., Carrozzo R., Patel K., Sheer D., Lehrach H.,
 RA North M.A.;
 RT "Olfactory receptor gene cluster on human chromosome 17: possible
 RT duplication of an ancestral receptor repertoire.",
 RL Hum. Mol. Genet. 3:229-235(1994).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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DR EMBL: U04687; AAA18350.1; -

DR GCRDB: GCR_0854; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; FALSE_NEG.

DR PROSITE: PS00262; G_PROTEIN_RECIP_FL_2; 1.

DR G-protein coupled receptor: Transmembrane; glycoprotein;

DR Multigene family: Olfaction.

FT NON_TER 1 1

FT TRANSMEM <1 12 2 (POTENTIAL).

FT DOMAIN 13 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 53 3 (POTENTIAL).

FT DOMAIN 54 72 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 74 91 4 (POTENTIAL).

FT DOMAIN 92 129 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 130 153 5 (POTENTIAL).

FT DOMAIN 154 170 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 171 194 6 (POTENTIAL).

FT DOMAIN 195 205 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 206 >216 7 (POTENTIAL).

FT NON_TER 216 216

FT SEQUENCE 216 AA; 23617 MW; 28DBCBE3973F9F2 CRC64;

Query Match

Best Local Similarity 4.3%; Score 7; DB 1; Length 216;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 KAFSTCG 119

DB 169 KAFSTCG 175

RESULT 14

OL1L_HUMAN STANDARD; PRT; 216 AA.

AC P47892;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Olfactory receptor-like protein OR17-219 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94272458; PubMed=8004088;
RA Ben-Arie N., Lancet D., Taylor C., Khem N., Walker N.,
RA Ledbetter D.H., Carrozzo R., Patel K., Sheer D., Lehrach H.,
RA North M.A.,
RT "Olfactory receptor gene cluster on human chromosome 17: possible
RT duplication of an ancestral receptor repertoire.";
RL Hum. Mol. Genet. 3:229-235(1994).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: U04691; AAA18354.1; -

DR GCRDB: GCR_0858; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; 1.

DR PROSITE: PS00262; G_PROTEIN_RECIP_FL_2; 1.

DR G-protein coupled receptor: Transmembrane; glycoprotein;

DR Multigene family: Olfaction.

FT NON_TER 1 1

FT TRANSMEM <1 12 2 (POTENTIAL).

FT DOMAIN 13 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 53 3 (POTENTIAL).

FT DOMAIN 54 72 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 74 91 4 (POTENTIAL).

FT DOMAIN 92 129 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 130 153 5 (POTENTIAL).

FT DOMAIN 154 170 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 171 194 6 (POTENTIAL).

FT DOMAIN 195 205 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 206 >216 7 (POTENTIAL).

FT NON_TER 216 216

FT SEQUENCE 216 AA; 23613 MW; 74449CEC8C73144C CRC64;

Query Match

Best Local Similarity 4.3%; Score 7; DB 1; Length 216;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 KAFSTCG 119

DB 169 KAFSTCG 175

RESULT 15

OLF6_MOUSE STANDARD; PRT; 222 AA.

AC P34386;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Olfactory receptor 6 (M50) (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver;
RA Ressler K.J., Sullivan S.L., Buck L.B.,
RA "A zonal organization of odorant receptor gene expression in the
RT olfactory epithelium.";
RL Cell 73:597-609(1993).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: I14567; AAA39851.1; -

DR PIR: B40745; B40745.

DR GCRDB: GCR_0714; -

DR MGD: MGI:104713; Olf6.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; 1.

DR PROSITE; PS50262; G-PROTEIN_RECIP_F1_2; 1.
 KW G-Protein coupled receptor; Transmembrane; Multigene family;
 OLfaction.
 FT NON_TER 1 1
 FT TRANSMEM <1 19 2 (POTENTIAL).
 FT DOMAIN 20 40 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 41 60 3 (POTENTIAL).
 FT DOMAIN 61 79 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 98 4 (POTENTIAL).
 FT DOMAIN 99 136 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 137 159 5 (POTENTIAL).
 FT DOMAIN 160 176 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 177 200 6 (POTENTIAL).
 FT DOMAIN 201 212 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 213 >222 7 (POTENTIAL).
 FT NON_TER 222 222
 SQ SEQUENCE 222 AA; 24748 MW; 7235CEDDDDEA3BE7 CRC64;

Query Match 4.3%; Score 7; DB 1; Length 222;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 IFMYVRP 139
 |||||
 Db 196 IFMYVRP 202

Search completed: June 27, 2002, 14:17:10
 Job time: 252 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 27, 2002, 14:12:23 ; search time 23.9 Seconds
(without alignments)
1172.602 Million cell updates/sec

Title: US-09-747-155-225

Perfect score: 162
Sequence: 1 VAICNPDLPLYPVWMSNKLKSAQ.....LAEDQDKVSYLFTIITLPL 162

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SPTRMBL_19:*

1: sp_archaea:*\n2: sp_bacteria:*\n3: sp_fungi:*\n4: sp_human:*\n5: sp_invertebrate:*\n6: sp_mammal:*\n7: sp_mhc:*\n8: sp_organelle:*\n9: sp_phage:*\n10: sp_plant:*\n11: sp_protent:*\n12: sp_virus:*\n13: sp_vertebrate:*\n14: sp_unclassified:*\n15: sp_virus:*\n16: sp_bacteriap:*\n17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	162	4	Q9NZP5
2	162	45.7	162	6	Q9N1M1
3	162	6.2	162	6	Q9N1M1
4	162	6.2	221	11	Q9Z230
5	162	6.2	309	11	Q9EOA6
6	162	6.2	309	11	Q9EOA4
7	162	6.2	314	11	Q9EOA5
8	162	6.2	315	6	Q9TSM7
9	162	6.2	157	4	Q15614
10	162	6.2	157	4	Q15617
11	162	6.2	157	6	Q28307
12	162	6.2	157	11	Q63595
13	162	6.2	161	6	Q9N1G5
14	162	6.2	161	6	Q9N1N3
15	162	6.2	162	6	Q9N1L5
16	162	6.2	162	6	Q9N1L0

17	9	5.6	162	6	Q9N1J9	Q9n1j9 macaca sylv
18	9	5.6	162	6	Q9N1J2	Q9n1j2 callithrix
19	9	5.6	162	6	Q9N1I9	Q9n1i9 callithrix
20	9	5.6	162	6	Q9N1H0	Q9n1h0 salmirl sci
21	9	5.6	162	6	Q9N1G2	Q9n1g2 salmirl bol
22	9	5.6	214	11	Q9JM36	Q9jm36 mus musculu
23	9	5.6	215	4	Q96R00	Q96rc0 homo sapien
24	9	5.6	215	4	Q96RC9	Q96rc9 homo sapien
25	9	5.6	215	4	Q96RC6	Q96rc6 homo sapien
26	9	5.6	216	4	Q96RC8	Q96rc8 homo sapien
27	9	5.6	216	4	Q96RC2	Q96rc2 homo sapien
28	9	5.6	216	4	Q96RB5	Q96rb5 homo sapien
29	9	5.6	216	4	Q96RB4	Q96rb4 homo sapien
30	9	5.6	216	4	Q96RB2	Q96rb2 homo sapien
31	9	5.6	216	4	Q96RB2	Q96rb2 homo sapien
32	9	5.6	216	11	Q9JM27	Q9jm27 mus musculu
33	9	5.6	217	4	Q96RC7	Q96rc7 homo sapien
34	9	5.6	217	4	Q96RC3	Q96rc3 homo sapien
35	9	5.6	217	4	Q96RC3	Q96rc3 homo sapien
36	9	5.6	221	11	Q9Z236	Q9z236 rattus norv
37	9	5.6	221	11	Q9Z231	Q9z231 rattus norv
38	9	5.6	223	11	Q9Z1V5	Q9z1v5 mus musculu
39	9	5.6	304	11	Q9QW36	Q9qw36 rattus sp.
40	9	5.6	306	11	Q9EO89	Q9eq89 mus musculu
41	9	5.6	307	11	Q9EO96	Q9eq96 mus musculu
42	9	5.6	309	11	Q9EOG1	Q9eqg1 mus musculu
43	9	5.6	309	11	Q9EBO6	Q9ebu6 mus musculu
44	9	5.6	310	11	Q9EOB0	Q9ebu0 mus musculu
45	9	5.6	310	11	Q9EOA7	Q9eqa7 mus musculu

ALIGNMENTS

RESULT	ID	Q9NZP5	PRELIMINARY:	PRT:	162 AA.
AC	Q9NZP5	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	OLFACTORY RECEPTOR (FRAGMENT).				
GN	HSAL				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20183981; PubMed=10706615;				
RA	Rouquier S., Blancher A., Giorgi D.;				
RT	"The olfactory receptor gene repertoire in primates and mouse:				
RT	Evidence for reduction of the functional fraction in primates.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).				
DR	EMBL: AF179759; AAF40348.1; -				
DR	InterPro: IPR000276; GPCr_Rhodopsn.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PROSITE: PS50262; G_PROTEIN_RECPT_F1.2; 1.				
KW	Receptor.				
FT	NON_TER	1			
FT	NON_TER	162			
FT	SEQUENCE	162 AA; 18386 MW; 6716C48C3ED0E4D8 CRC64;			

Query Match 100.0%; Score 162; DB 4; Length 162;
Best local Similarity 100.0%; Pred. No. 2.9e-162;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VAICNPDLPLYPVWMSNKLKSAQLSISYVIGFLPLVHVSLLRLTFCGRFNIHIFYEIIQ 60
DB	1	VAICNPDLPLYPVWMSNKLKSAQLSISYVIGFLPLVHVSLLRLTFCGRFNIHIFYEIIQ 60
QY	61	LFRLSCNGPSINMLIFIFGCAFIQIPLMTIISYTRVLPDLILKKSEKGRKAFSTGCA 120

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Db 61 LFKISCNPSINALIFFGAFIQIPTLMTIISTYTRVLPDILKKSEKRSKAFSTCGA 120
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162

RESULT 2
09N1M1 PRELIMINARY: PRT; 162 AA.
AC 09N1M1: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTOR RECEPTOR (FRAGMENT).
GN PTR210.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
DR EMBL: AF179735; AAF40330.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PSS0262; G_PROTEIN_RECPE_FL_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 162 162
SQ SEQUENCE 162 AA; 18389 MW; 586280CC7BD5F4CE CRC64;

Query Match 45.7%; Score 74; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAICNPPLLYPMMSNKSIAQLISIVYIGFLPLVHVSLLRLTFPCRNIIHYECILQ 60
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
Db 1 VAICNPPLLYPMMSNKSIAQLISIVYIGFLPLVHVSLLRLTFPCRNIIHYECILQ 60
QY 61 LFKISCNPSINAL 74
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
Db 61 LFKISCNPSINAL 74

RESULT 3
09N1M1 PRELIMINARY: PRT; 162 AA.
AC 09N1M1: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTOR RECEPTOR (FRAGMENT).
GN PPA138.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183981; PubMed=10706615;
RA Rouquier S., Blancher A., Giorgi D.;
RT "The olfactory receptor gene repertoire in primates and mouse:
RT Evidence for reduction of the functional fraction in primates.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
DR EMBL: AF179721; AAF40317.1; -;

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DR InterPro: IPR000276; GPCR_Rhodpsn.
DR PROSITE: PSS0262; G_PROTEIN_RECPE_FL_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 162 162
SQ SEQUENCE 162 AA; 18112 MW; ACD9BA1ECBD37959 CRC64;

Query Match 6.2%; Score 10; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 KAFSTCGAHL 122
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
Db 113 KAFSTCGAHL 122

RESULT 4
092230 PRELIMINARY: PRT; 221 AA.
AC 092230: 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTOR RECEPTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HFL-VNI;
RA Singer M.S., Hughes T.E., Shepherd G.M., Greer C.A.;
RT "Isolation of olfactory receptor mRNA sequences from olfactory bulb
RT glomerular layer.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF091576; AAC64596.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PSS00237; G_PROTEIN_RECPE_FL_1; UNKNOWN_1.
DR PROSITE: PSS0262; G_PROTEIN_RECPE_FL_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 221 221
SQ SEQUENCE 221 AA; 24719 MW; 1FF1BF090F84E4C1 CRC64;

Query Match 6.2%; Score 10; DB 11; Length 221;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 KGRSKAFSTC 118
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
    121 HLVSLSLYGTFIMYVPASGLAEDODKYSLPYTIIIPLL 162
Db 169 KGRSKAFSTC 178

RESULT 5
09EOA6 PRELIMINARY: PRT; 309 AA.
AC 09EOA6: 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTOR RECEPTOR K25.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ;
RX MEDLINE=21015403; PubMed=11130974;

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RA Xie S.Y., Feinstein P., Mombaerts P.;
 RT "Characterization of a Cluster Comprising 100 Odorant Receptor Genes
 in Mouse.";
 RL Mamm. Genome 11:1070-1078(2000).
 DR EMBL; AF282283; AAG39868.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 309 AA; 34645 MW; A07D06336AEF837 CRC64;

Query Match 6.2%; Score 10; DB 11; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTCG 119
 |||||
 Db 232 GRSKAFSTCG 241

RESULT 6
 O9EOA4 PRELIMINARY; PRT; 309 AA.
 AC O9EOA4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ODORANT RECEPTOR K27.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=21015403; PubMed=11130974;
 RA Xie S.Y., Feinstein P., Mombaerts P.;
 RT "Characterization of a Cluster Comprising 100 Odorant Receptor Genes
 in Mouse.";
 RL Mamm. Genome 11:1070-1078(2000).
 DR EMBL; AF282283; AAG39870.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam; PR00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 309 AA; 34592 MW; D58DA04AFDE88DD CRC64;

Query Match 6.2%; Score 10; DB 11; Length 309;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTCG 119
 |||||
 Db 232 GRSKAFSTCG 241

RESULT 7
 O9EOA5 PRELIMINARY; PRT; 314 AA.
 AC O9EOA5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ODORANT RECEPTOR K26.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=21015403; PubMed=11130974;
 RA Xie S.Y., Feinstein P., Mombaerts P.;
 RT "Characterization of a Cluster Comprising 100 Odorant Receptor Genes
 in Mouse.";
 RL Mamm. Genome 11:1070-1078(2000).
 DR EMBL; AF282284; AAG39869.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 35120 MW; 4D1C19E3ABEDD439 CRC64;

Query Match 6.2%; Score 10; DB 11; Length 314;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTCG 119
 |||||
 Db 237 GRSKAFSTCG 246

RESULT 8
 O9TSM7 PRELIMINARY; PRT; 315 AA.
 AC O9TSM7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE OLFACTORY RECEPTOR.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxId=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MF0R1P1;
 RX MEDLINE=9443869; PubMed=10512677;
 RA Sharon D., Glusman G., Pilpel Y., Khen M., Gruetznr F., Haaf T.,
 RT "Primate evolution of an olfactory receptor cluster: diversification
 by gene conversion and recent emergence of pseudogenes.";
 RL Genomics 61:24-36(1999).
 DR EMBL; AF101778; AAF03348.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam; PR00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS50237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 315 AA; 34638 MW; 778E19FBA03F646C CRC64;

Query Match 6.2%; Score 10; DB 6; Length 315;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 KAFSTCAHL 122
 |||||
 Db 239 KAFSTCAHL 248

RESULT 9
 O15614 PRELIMINARY; PRT; 157 AA.
 AC O15614;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE PUTATIVE OLFACTORY RECEPTOR (FRAGMENT).
GN TPCR120.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE=97224452; PubMed=9119360;
RA Vanderhaeghen P., Schumann S., Vassart G., Parmentier M.;
RT "Specific repertoire of olfactory receptor genes in the male germ
cells of several mammalian species.";
RL Genomics 39:239-246(1997).
DR EMBL: X89669; CA61816.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PSS0262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 157 AA; 17300 MW; 64B3DD9A484D1E55 CRC64;
SQ

Query Match 5.6%; Score 9; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTC 118
Db 108 GRSKAFSTC 116

RESULT 10
ID 015617 PRELIMINARY; PRT; 157 AA.
AC 015617;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE OLFACTORY RECEPTOR (FRAGMENT).
GN TPCR25.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE=97224452; PubMed=9119360;
RA Vanderhaeghen P., Schumann S., Vassart G., Parmentier M.;
RT "Specific repertoire of olfactory receptor genes in the male germ
cells of several mammalian species.";
RL Genomics 39:239-246(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC Fuchs T., Moleceva B., Linhart C., Sharan R., Khen M., Herwig R.,
RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radloff U.,
RA Lebrach H., Olander Z., Giesman G., Lancel D., Shamir R.;
RT "DEPOS: A Practical Scheme for Deciphering Families of Genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: X89672; CA61819.1; -;
DR EMBL: AF399507; AAK94992.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR PROSITE: PSS0262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 157 AA; 17264 MW; 0F73893D7D2A2E04 CRC64;
SQ

Query Match 5.6%; Score 9; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 110 GRSKAFSTC 118
Db 108 GRSKAFSTC 116

RESULT 11
ID 028307 PRELIMINARY; PRT; 157 AA.
AC 028307;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE OLFACTORY RECEPTOR (FRAGMENT).
GN TPCR79.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE=97224452; PubMed=9119360;
RA Vanderhaeghen P., Schumann S., Vassart G., Parmentier M.;
RT "Specific repertoire of olfactory receptor genes in the male germ
cells of several mammalian species.";
RL Genomics 39:239-246(1997).
DR EMBL: X89665; CA61812.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PSS0262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 157 AA; 17236 MW; BEC0C82DB37A6AAD CRC64;
SQ

Query Match 5.6%; Score 9; DB 6; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTC 118
Db 108 GRSKAFSTC 116

RESULT 12
ID 063595 PRELIMINARY; PRT; 157 AA.
AC 063595;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE OLFACTORY RECEPTOR (FRAGMENT).
GN TPCR21.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE=97224452; PubMed=9119360;
RA Vanderhaeghen P., Schumann S., Vassart G., Parmentier M.;
RT "Specific repertoire of olfactory receptor genes in the male germ
cells of several mammalian species.";
RL Genomics 39:239-246(1997).
DR EMBL: X89704; CA61851.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PSS0262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.

FT NON_TER 1 1
 FT NON_TER 157 157
 SO SEQUENCE 157 AA; 17653 MW; 84724899D60CB049 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 9; DB 11; Length 157;
 Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTC 118
 DB 108 GRSKAFSTC 116

RESULT 13

ID 09NIG5 PRELIMINARY; PRT; 161 AA.

AC 09NIG5; 01-OCT-2000 (TREMBLREL. 15, Created)

DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)

DE 01-JUN-2001 (TREMBLREL. 17, Last annotation update)

OC OLFACTORY RECEPTOR (FRAGMENT).

GN SBO218.

OS Saimiri boliviensis (Bolivian squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.

NCBI_TaxID=27679;

[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20183981; PubMed=10706615;

RA Rouquier S., Blancher A., Giorgi D.;

RT "The olfactory receptor gene repertoire in primates and mouse;

RT Evidence for reduction of the functional fraction in primates.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).

DR EMBL; AF179756; AAF40346.1;

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECCEP_FL_2; 1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 161 161

SO SEQUENCE 161 AA; 17370 MW; 44616DD51F73E81 CRC64;

Query Match

Best Local Similarity 100.0%; Score 9; DB 6; Length 161;

Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPLY 9

DB 1 VAICNPLY 9

RESULT 14

ID 09NIN3 PRELIMINARY; PRT; 162 AA.

AC 09NIN3; 01-OCT-2000 (TREMBLREL. 15, Created)

DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)

DE 01-JUN-2001 (TREMBLREL. 17, Last annotation update)

OC OLFACTORY RECEPTOR (FRAGMENT).

GN PPA139.

OS Papio hamadryas (Hamadryas baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Papio.

NCBI_TaxID=9557;

[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20183981; PubMed=10706615;

RA Rouquier S., Blancher A., Giorgi D.;

RT "The olfactory receptor gene repertoire in primates and mouse;

RT Evidence for reduction of the functional fraction in primates.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).

DR EMBL; AF179722; AAF40318.1;

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECCEP_FL_2; 1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 162 162

SO SEQUENCE 162 AA; 18082 MW; 44E77F9E7E4373D4 CRC64;

Query Match

Best Local Similarity 100.0%; Score 9; DB 6; Length 162;

Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VAICNPLY 9

DB 1 VAICNPLY 9

RESULT 15

ID 09N1L5 PRELIMINARY; PRT; 162 AA.

AC 09N1L5; 01-OCT-2000 (TREMBLREL. 15, Created)

DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)

DE 01-JUN-2001 (TREMBLREL. 17, Last annotation update)

OC OLFACTORY RECEPTOR (FRAGMENT).

GN GGO107.

OS Gorilla gorilla (gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.

NCBI_TaxID=9593;

[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20183981; PubMed=10706615;

RA Rouquier S., Blancher A., Giorgi D.;

RT "The olfactory receptor gene repertoire in primates and mouse;

RT Evidence for reduction of the functional fraction in primates.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).

DR EMBL; AF179756; AAF40346.1;

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR PROSITE; PS50262; G_PROTEIN_RECCEP_FL_2; 1.

KW Receptor.

FT NON_TER 1 1

FT NON_TER 162 162

SO SEQUENCE 162 AA; 17360 MW; 76324350D05E53E6 CRC64;

Query Match

Best Local Similarity 100.0%; Score 9; DB 6; Length 162;

Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GRSKAFSTC 118

DB 110 GRSKAFSTC 118

Search completed: June 27, 2002, 14:16:38

Job time: 255 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 27, 2002, 11:17:07 ; Search time 1624.99 seconds
(without alignments)
4044.959 Million cell updates/sec

Title: US-09-747-155-224

Perfect score: 487
Sequence: 1 tgtagccatagtatccct.....cgattataatccctcgtcta 487

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 674847542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST.*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlma:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	4.3	389	10	BM253378
C 2	21	4.3	496	10	BE752648
C 3	20	4.1	281	9	BB579415
C 4	20	4.1	408	10	BE991812
C 5	20	4.1	669	12	AG102096
C 6	20	4.1	811	12	AO270566
C 7	19	3.9	279	9	AA688627
C 8	19	3.9	300	9	AV176153
C 9	19	3.9	320	10	BE523391
C 10	19	3.9	327	9	AA611944
C 11	19	3.9	348	9	BE148808
C 12	19	3.9	355	10	BG733743
C 13	19	3.9	371	12	AO241320
C 14	19	3.9	378	10	M79761
C 15	19	3.9	408	9	AM835801
C 16	19	3.9	408	12	AO593534
C 17	19	3.9	410	9	AM835811

C 18	19	3.9	410	12	AO674479
C 19	19	3.9	423	9	AM862208
C 20	19	3.9	447	9	AM453392
C 21	19	3.9	447	10	BI034798
C 22	19	3.9	452	10	BI497566
C 23	19	3.9	467	12	BH298263
C 24	19	3.9	477	9	AM871068
C 25	19	3.9	496	12	AZ366926
C 26	19	3.9	502	9	A1605706
C 27	19	3.9	513	9	AV526912
C 28	19	3.9	528	12	BH008916
C 29	19	3.9	542	9	AM941540
C 30	19	3.9	566	12	AZ874840
C 31	19	3.9	607	12	AO548864
C 32	19	3.9	629	9	AM384082
C 33	19	3.9	641	12	BH291135
C 34	19	3.9	655	12	AZ086983
C 35	19	3.9	655	12	AG151658
C 36	19	3.9	698	10	BJ134615
C 37	19	3.9	714	10	BE618995
C 38	19	3.9	933	12	CNS04ZKO
C 39	19	3.9	957	12	CNS05J69
C 40	19	3.9	964	12	AO899367
C 41	18	3.7	150	10	BI052471
C 42	18	3.7	158	9	BE014092
C 43	18	3.7	162	12	AZ113993
C 44	18	3.7	179	10	M79844
C 45	18	3.7	205	9	BE172103

ALIGNMENTS

RESULT 1
LOCUS BM253378
DEFINITION 514417 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM253378
VERSION
KEYWORDS
SOURCE
ORGANISM Bos taurus
COW.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
1 (bases 1 to 389)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitto-McKown,C.G., Pertea,G., Holt,I., Karanaycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCATCAGCAGC
Plate: 110 row: F column: 4
Seq primer: ATTTAGTGACACTATGAC.
Location/Qualifiers
1. 389
/organism="Bos taurus"
/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
longissimus muscle." 130 a 51 c 61 g 147 t

BASE COUNT 130 a 51 c 61 g 147 t

ORIGIN

Query Match 4.3%; Score 21; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 ttattttgtgtgtttata 250
|||||
Db 64 TTTATTTTGTGCTTTTATA 44

RESULT 2
BE752648 496 bp mRNA linear EST 25-APR-2001
LOCUS BE752648
DEFINITION 205097 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE752648
VERSION BE752648.1 GI:10166640
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 496)
Smith, T. P. L., Grose, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,
Casas, E., May, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett,
G. L., Heaton, M. P., Laegreid, W. M., Rohrer, G. A., Chitko-McCown, C. G.,
Perte, G., Holt, I., Karanycheva, S., Liang, F., Quackenbush, J., and
Keefe, J. W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt. trimmed with phred
v0.960904.e. Vector identified by cross-match with the -m1nscore 18
and -m1match 12 options.
PCR Primers
FORWARD: AGGAACACGATGACCA
BACKWARD: GTTTCACGACGACG
Plate: 53 row: F column: 16
Seq primer: ATTACGACGACGATAG.
Location/Qualifiers
1. .496
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 171 a 66 c 81 g 178 t

ORIGIN

Query Match 4.3%; Score 21; DB 10; Length 496;
Best Local Similarity 100.0%; Pred. No. 8.7;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 ttattttgtgtgtttata 250
|||||
Db 156 TTTATTTTGTGCTTTTATA 136

RESULT 3
BB579415 281 bp mRNA linear EST 30-NOV-2000
LOCUS BB579415
DEFINITION BB579415 RIKEN full-length enriched, 11 days embryo gonad Mus
musculus cDNA clone 7030401H04 5', mRNA sequence.
ACCESSION BB579415
VERSION BB579415.1 GI:11475362
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 281)
Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P.,
Hanagaki, T., Hayatsu, N., Hirooka, T., Hirozane, T., Hodozawa, Y.,
Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Kono,
H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, H., Nishi, K.,
Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, K.,
Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A.,
Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka,
T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshiki, A., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Thermostabilization and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y., and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
Location/Qualifiers
1. .281
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="7030401H04"
/clone_lib="RIKEN full-length enriched, 11 days embryo
gonad"
/sex="mixed"
/tissue_type="gonad"
/dev_stage="11 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was

from mouse hippocampus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at brainrest.eng.uiowa.edu.

Query Match	4.1%	Score 20;	DB 10;	Length 408;
Best Local Similarity	100.0%	Pred. No. 29;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	303	atatctcgaaaaaagctc	322	
Db	377	ATATCTCGAAAAAAGTCT	396	

[illegible]

REFERENCE AUTHORS	1 (sites) Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE	BAC end Sequences of Library FTB
JOURNAL	Unpublished
REFERENCE AUTHORS	2 (bases 1 to 669) Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

JOURNAL
Submitted (02-Aug-2001) Asao Fujiwara, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC): 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: shiimbases@gsc.riken.go.jp, URR: <http://hnp.gsc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT
Clones are derived from the chimpanzee BAC library PTB this BAC end was generated during the Red process and may have higher chance of clone tracking errors.
PRIMERS

Sequencing: M13Rev
LIBRARY

FEATURES	Location/Qualifiers
source	1. .669

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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-105E20.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
243 a 93 c 164 g 167 t 2 others
BASE COUNT
ORIGIN

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Query Match	4.1%	Score 20:	DB 12	Length 669
Best Local Similarity	100.0%	Pred. No. 27		
Matches	20	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	308	ctgaataaaagtctgaana	327	
DB	75	ctgaataaaagtctgaana	94	

RESULT 6
 LOCUS AQ270566/c 811 bp DNA linear GSS 03-NOV-1998
 DEFINITION HS_2046_B1_F06_T7 CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=2046 Col=11 Row=L, DNA sequence.
 ACCESSION AQ270566
 VERSION AQ270566.1 GI:3823161
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 811)
 Maitres, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahatras GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 2046 row: L column: 11
 Class: BAC ends
 High quality sequence stop: 811.
 Location/Qualifiers
 1..811
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBel0BAC11; BAC Clones in
 E-Coli DH10B"
 BASE COUNT 236 a 178 c 132 g 264 t 1 others
 ORIGIN
 Query Match 4.1%; Score 20; DB 12; Length 811;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 165 actgtgaatttaccactg 184
 ||||||||||||||||||
 Db 523 ACTGTGAATTTTACACTG 504
 RESULT 7
 LOCUS AA689627/c 279 bp mRNA linear EST 16-DEC-1997
 DEFINITION v808h1.1 Barstead mouse irradiated colon MRLB7 Mus musculus CDNA
 clone IMAGE:1137669 5', mRNA sequence.
 ACCESSION AA689627
 VERSION AA689627.1 GI:2690563
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 279)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The Washu-HMI Mouse EST Project
 JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
 Washu-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LBNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:618941
 putative full length read
 vector to vector length is 280
 Seq primer: -28m13 rev2 EF from Amersham.
 Location/Qualifiers
 1..279
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 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:1137669"
 /clone_lib="Barstead mouse irradiated colon MRLB7"
 /dev_stage="8 weeks"
 /lab_host="DH10B"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker. Site_1: EcoRI; Site_2: NotI; Tissue obtained
 from 8 week old mouse. Colon was harvested 72 hours after
 irradiation with 1400 Gys. 1st strand cDNA was primed
 with a Not I - oligo(dT) primer
 [5'TGTACGAATCGAAGTGGAGCGGCCCGCTTTTCTTTTCTTTTCTTTTCTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors [AATTCGATCCTT], digested with Not I and cloned
 into the Not I and Eco RI sites of the modified p773
 vector. Library constructed by Bob Barstead."
 BASE COUNT 91 a 44 c 49 g 95 t
 ORIGIN
 Query Match 3.9%; Score 19; DB 9; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 469 gattataattccctgcta 487
 ||||||||||||||||||
 Db 92 GATTATAATTCCTCGCTA 74
 RESULT 8
 LOCUS AV176153 300 bp mRNA linear EST 21-JUL-1999
 DEFINITION AV176153 Yui1 Kohara unpublished cDNA:Strain N2 hermaphrodite
 embryo Caenorhabditis elegans cDNA clone yk508f9 3', mRNA sequence.
 ACCESSION AV176153
 VERSION AV176153.1 GI:5556054
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabdilitoidea
 ; Rhabdilitae; Peloderae; Caenorhabditis.
 1 (bases 1 to 300)
 Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H.,
 Nishigaki, A., Mochizashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano
 M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
 Nomoto, H.
 TITLE Expressed genes in C.elegans
 JOURNAL Unpublished (1999)
 COMMENT Contact: Yui1 Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.
 Location/Qualifiers
 1..300

```

/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk508f9"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT      144 a      23 c      52 g      71 t      10 others
ORIGIN

Query Match      3.9%; Score 19; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 gatattctgaaaaaagt 320
|||||
Db 11 GATATTCTGAAAAAAGT 29

RESULT 9
BE523391/c 320 bp mRNA linear EST 19-MAR-2001
LOCUS M36D6STM Arabidopsis developing seed Arabidopsis thaliana cDNA
DEFINITION clone M36D6 5', mRNA sequence.
ACCESSION BE523391
VERSION BE523391.1 GI:9781369
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 320)
White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
20567808

JOURNAL
MEDLINE
COMMENT Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
, USA
Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 305 Botany &
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
Location/Qualifiers
1. .320
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="M36D6"
/clone_lib="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"

BASE COUNT      86 a      53 c      88 g      92 t      1 others
ORIGIN

Query Match      3.9%; Score 19; DB 10; Length 320;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 7 catatgtaaccctgctt 25
|||||
Db 195 CATATGTAATCCCTGCTT 177

RESULT 10
AA611944 327 bp mRNA linear EST 01-OCT-1997
LOCUS AA611944/c
DEFINITION v086c02.r1 Barstead mouse irradiated colon MPLR87 Mus musculus cDNA
clone IMAGE:1065986 5', mRNA sequence.
ACCESSION AA611944
VERSION AA611944.1 GI:2461979
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 327)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:588346
Putative full length read
vector to vector length is 330
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 297.
Location/Qualifiers
1. .327
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1065986"
/clone_lib="Barstead mouse irradiated colon MPLR87"
/dev_stage="8 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained
from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gys. 1st strand cDNA was primed
with a Not I - oligo(dT) primer
[5'TGTTCAGCAATCGAATCGAGGAGCGCCGCCCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (AATTCGATCCTTG), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library constructed by Bob Barstead. "

BASE COUNT      105 a      51 c      57 g      114 t
ORIGIN

Query Match      3.9%; Score 19; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 469 gattataatccctgcta 487
|||||
Db 138 GATTATAATCCCTGCTA 120

RESULT 11
BE148808

```

LOCUS BE148808 348 bp mRNA linear EST 21-JUN-2000
DEFINITION CM4-HT0243-081199-037-a06 HT0243 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE148808
VERSION BE148808.1 GI:8611532
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,
Nagai, M.A., da Silva, M.J., Zago, M.A., Bordin, S., Costa, F.F.,
Golman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-CM4-HT0243-081
199-037-a06&t3=1999-11-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 30
High quality sequence stop: 348.
FEATURES
Source Location/Qualifiers
1..348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="HT0243"
/dev_stage="Adult"
/note="Organ: head-neck; Vector: puc18; Site:1: Sma1;
Site:2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent applica-
tion No. 196,716 - Ludwig Institute for Cancer Research)
Profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 76 a 60 c 77 g 135 t
ORIGIN
Query Match 3.9%; Score 19; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 73 ttcacatgtaattggttc 91
|||||
Db 301 ttcacatgtaattggttc 319
RESULT 12
Bg733743 355 bp mRNA linear EST 11-MAY-2001
LOCUS Bg733743
DEFINITION As.nc.01H01.SKPL Ascaris suum (parasitic nematode) adult nerve cord
and muscle Ascaris suum cDNA clone As_nc_01H01.5' similar to
ref|NP_006951.1|ND3.10020 NADH dehydrogenase subunit 3 - Ascaris
suum, mRNA sequence.
ACCESSION Bg733743
VERSION Bg733743.1 GI:14020027
KEYWORDS EST.
SOURCE plg roundworm.
ORGANISM Ascaris suum

Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea
; Ascarididae; Ascaris.
REFERENCE 1 (bases 1 to 355)
AUTHORS Blaxter, M.L., Parkinson, J., Whitton, C., Daub, J., Guiliano, D., Hall,
N., Quayle, M. and Barrell, B.
Edinburgh University/Sanger Centre Nematode EST Project
Unpublished (2000)
COMMENT Contact: Blaxter M.
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JF, UK.
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
The library was prepared for Dr Tim Geary, Upjohn Laboratories,
Kalamazoo, MI, USA Sequencing was performed by Claire Whitton ICAPB,
Edinburgh The sequence contained a PolyA tail (trimmed)
PCR Primers
FORWARD: T73
BACKWARD: T7PL
Plate: 01 row: H column: 01
Seq primer: SKPL
High quality sequence stop: 355.
FEATURES
Source Location/Qualifiers
1..355
/organism="Ascaris suum"
/db_xref="taxon:6253"
/clone="As.nc.01H01"
/clone_1lb="Ascaris suum (parasitic nematode) adult nerve
cord and muscle"
/sex="mixed"
/tissue_type="nerve cord and associated muscle"
/dev_stage="adult"
/note="Vector: lambda zap II; Site:1: EcoRI (5'end);
Site:2: EcoRI (3'end); Ascaris suum is an intestinal
nematode parasite of pigs. The library was constructed
from dissected nerve cord and associated muscle tissue for
Dr. T. Geary, Pharmacia-Upjohn Inc, Kalamazoo, MI, USA
[tgeary@am.pnu.com]"
BASE COUNT 68 a 15 c 78 g 194 t
ORIGIN
Query Match 3.9%; Score 19; DB 10; Length 355;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 224 ataatattatttgggtg 242
|||||
Db 292 ataatattatttgggtg 310
RESULT 13
A0241320 371 bp DNA linear GSS 30-SEP-1998
LOCUS A0241320/c
DEFINITION CITBI-EI-2501016.TF.1 CITBI-EI Homo sapiens genomic clone 2501016,
DNA sequence.
ACCESSION A0241320
VERSION A0241320.1 GI:3673153
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 371)
AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
Venter, J.C.
TITLE Use of a random human BAC End sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CITBI-EI-2501016.TF.1

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES

source

1.371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="2501016"
/clone_lib="CITBT-El"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 96 a 76 c 103 g 96 t
ORIGIN

Query Match 3.9%; Score 19; DB 12; Length 371;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 catgtgagttactcttcgc 125
|||||
Db 294 CATGTGAGTTACTCTTCGC 276

RESULT 14

LOCUS

M79761 378 bp mRNA linear EST 30-JUN-1992
WEST00298 Mixed stage, Striatogene (cat. #937006) Caenorhabditis
elegans cDNA clone CEMSD32, mRNA sequence.

ACCESSION

VERSION

M79761
M79761.1 GI:271780

KEYWORDS

SOURCE

Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1 (bases 1 to 378)
Rhabditidae; Feloderinae; Caenorhabditis.
McCombie, W.R., Adams, M.D., Kelley, J.M., Fitzgerald, M.G., Utterback,
T.R., Khan, M., Dubnick, M., Kerlavage, A.R., Venter, J., and Fields, C.

REFERENCE

AUTHORS

Caenorhabditis elegans expressed sequence tags identify gene
families and potential disease gene homologues
Nature Genet. 1, 124-131 (1992)

JOURNAL

MEDLINE

93250983
Contact: Kerlavage, AR

COMMENT

Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
Seq primer: M13 forward.
Location/Qualifiers

FEATURES

source

1.378
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone_lib="CEMSD32"
/clone_lib="Mixed stage, Striatogene (cat. #937006)"
/note="Vector: Uni-ZAP XR; C. elegans mixed stage cDNA
library. Striatogene catalog #937006. The library is oligo
df primed and directionally cloned in the Uni-ZAP XR
vector."
BASE COUNT 163 a 32 c 78 g 98 t 7 others

ORIGIN

Query Match 3.9%; Score 19; DB 10; Length 378;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 302 gatattctgaaaaaagt 320
|||||
Db 43 GATATTCTGAAAAAAAGT 61

RESULT 15

LOCUS

AM835801 408 bp mRNA linear EST 18-MAY-2000
QV4-LT0016-240200-110-D12 LT0016 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM835801
VERSION AM835801.1 GI:7929775
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 408)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baig, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

20202663

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=at2-QV4-LT0016-240>)
200-110-D12&t3-2000-02-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 408.

FEATURES

source

Location/Qualifiers
1.408
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LT0016"
/dev_stage="Adult"
/note="Organ: leiomyos; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESSES PCR (O.S. letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 142 a 68 c 95 g 103 t
ORIGIN

Query Match

3.9%; Score 19; DB 9; Length 408;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 360

cccatctgcttctcttc 378
|||||

Db 342

CCCATCTGCTTCTCTTC 324

Thu Jun 27 14:54:40 2002

Search completed: June 27, 2002, 12:37:17
Job time: 4810 sec

us-09-747-155-224.oli.rst

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 27, 2002, 10:18:27 ; Search time 1791.3 Seconds
(without alignments)
5689.289 Million cell updates/sec

Title: US-09-747-155-224
Perfect score: 487
Sequence: 1 tgcagcatcatgtaaccctc.....cgattataatccctgcta 487

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_mu:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
------------	-------------	--------	-------	-------------

1	487	100.0	487	6	AX181436	AX181436 Sequence
2	487	100.0	487	9	AF179759	AF179759 Homo sapi
3	486	99.8	486	6	AX242110	AX242110 Sequence
4	477.4	98.0	487	6	AX181394	AX181394 Sequence
5	477.4	98.0	487	6	AF179735	AF179735 Pan trogl
6	465	95.5	485	6	AX181383	AX181383 Sequence
7	465	95.5	485	9	AF179729	AF179729 Pan trogl
8	319	65.5	988	6	AX241993	AX241993 Sequence
9	319	65.5	150083	2	AC024892	AC024892 Homo sapi
10	294	60.4	138556	2	AC105564	AC105564 Rattus no
11	291.8	59.9	693	10	AY074239	AY074239 Mus muscu
12	290.4	59.6	663	10	AF091575	AF091575 Rattus no
13	282.2	57.9	918	10	AY073096	AY073096 Mus muscu
14	282.2	57.9	921	10	AY073611	AY073611 Mus muscu
15	282.2	57.9	138556	2	AC105564	AC105564 Rattus no
16	281.2	57.7	927	10	AY073094	AY073094 Mus muscu
17	279	57.3	919	10	AY074074	AY074074 Mus muscu
18	279	57.3	921	10	AY073097	AY073097 Mus muscu
19	276.4	56.8	924	10	AY073093	AY073093 Mus muscu
20	266.2	54.7	537	10	AY074165	AY074165 Mus muscu
21	260.4	53.5	918	10	AY073708	AY073708 Mus muscu
22	255	52.4	930	10	AY073612	AY073612 Mus muscu
23	250.8	51.5	930	10	AY073315	AY073315 Mus muscu
24	250.4	51.4	916	10	AY074143	AY074143 Mus muscu
25	245.4	50.4	487	6	AX181367	AX181367 Sequence
26	245.4	50.4	487	9	AF179721	AF179721 Papio ham
27	242.2	49.7	942	6	AX241501	AX241501 Sequence
28	242.2	49.7	166267	2	AC025942	AC025942 Homo sapi
29	238	48.9	709	10	AY074075	AY074075 Mus muscu
30	237.4	48.7	930	10	AY073772	AY073772 Mus muscu
31	236	48.5	958	6	AX241532	AX241532 Sequence
32	236	48.5	166267	2	AC025942	AC025942 Homo sapi
33	229.4	47.1	972	6	AX241530	AX241530 Sequence
34	227.8	46.8	927	10	AY073771	AY073771 Mus muscu
35	225.2	46.2	930	10	AY073613	AY073613 Mus muscu
36	224.6	46.1	927	6	AX241526	AX241526 Sequence
37	220.4	45.3	816	10	AY074144	AY074144 Mus muscu
38	217	44.6	940	6	AX241523	AX241523 Sequence
39	210.2	43.2	944	6	AX241521	AX241521 Sequence
40	206.8	42.5	483	10	AY074077	AY074077 Mus muscu
41	202.2	41.5	909	10	AY073698	AY073698 Mus muscu
42	201	41.3	931	6	AX241503	AX241503 Sequence
43	189.4	38.9	927	10	AY073090	AY073090 Mus muscu
44	187.8	38.6	918	10	AY074076	AY074076 Mus muscu
45	171.8	35.3	927	10	AY073086	AY073086 Mus muscu

ALIGNMENTS

RESULT 1
AX181436 LOCUS AX181436
DEFINITION Sequence 224 from Patent WO0146262.
ACCESSION AX181436
VERSION AX181436.1 GI:15141548
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 487)
JOURNAL Rouquier, S. and Giorgi, D.
Olfactory receptor genes and pseudogenes in primates and mouse
Patent: WO 0146262-A 224 28-JUN-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
LOCATION/Qualifiers
1. 487
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Taxon = 9606; gene = HSA1; Accession
DBJ/EMBL/GenBank = AF179759"
CDs
CD5

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/codon_start=1
/product="Olfactory receptor"
/protein_id="CAC50218.1"
/db_xref="GI:15141549"
/translation="VAICNPILYPMVMSNKLSAOLLSIVYIGFLHPLVHSLRLT
PCRFNIHIFVCEIILQPKISGNPSINALIIFIGARIGIPTLMTIIISYRVLEDI
LKKSEKRSKSAFSTCGAHLISVLSIYGTILFMVYRPSGLAEODKVSLEYTIIIP
LT"
BASE COUNT      131 a      105 c      77 g      174 t
ORIGIN
Query Match      100.0%; Score 487; DB 6; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.5e-98;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ttagcgaatgtaaccccttgcttataccagtgatgagtcacaacactcagcgctca 60
OY 61 gtgtcgaatgtaaccccttgcttataccagtgatgagtcacaacactcagcgctca 120
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DB 61 gtgtcgaatgtaaccccttgcttataccagtgatgagtcacaacactcagcgctca 120
OY 121 attgcgaactactctcgaaggttaacatacattcttactcgtgaaatttaca 180
    |||||||
DB 121 attgcgaactactctcgaaggttaacatacattcttactcgtgaaatttaca 180
OY 181 actgttcaaatcttcgtgaatggttcacatacgaacataataattattttgg 240
    |||||||
DB 181 actgttcaaatcttcgtgaatggttcacatacgaacataataattattttgg 240
OY 241 tgcctttatatacaaaatccacttgaactcaataccttatacctcgtgctctt 300
    |||||||
DB 241 tgcctttatatacaaaatccacttgaactcaataccttatacctcgtgctctt 300
OY 301 tgaatctcgaaaaaaagtcgaagaaggcgaagaagccttcacatgcggcgc 360
    |||||||
DB 301 tgaatctcgaaaaaaagtcgaagaaggcgaagaagccttcacatgcggcgc 360
OY 361 ccatcgtcttctgtctcactgtactaaggaactcgaactcctcgtgagtcgtcgc 420
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DB 361 ccatcgtcttctgtctcactgtactaaggaactcgaactcctcgtgagtcgtcgc 420
OY 421 atcttgcttagctgaagacaaagatgtaattctcgttttcaacagatataatcc 480
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DB 421 atcttgcttagctgaagacaaagatgtaattctcgttttcaacagatataatcc 480
OY 481 cctgcta 487
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DB 481 cctgcta 487
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RESULT 2
AF179759 487 bp DNA linear PRI 09-MAR-2000
LOCUS      AF179759
DEFINITION Homo sapiens olfactory receptor (hSAI) gene, partial cds.
ACCESSION AF179759
VERSION    AF179759.1 GI:7211526
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS   Rouquier S., Blancher A. and Giorgi D.
TITLE     The olfactory receptor gene repertoire in primates and mouse:
            evidence for reduction of the functional fraction in primates
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2870-2874 (2000)
MEDLINE   20183981
REFERENCE 2 (bases 1 to 487)
AUTHORS   Giorgi D.G. and Rouquier S.P.
TITLE     Direct Submission

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JOURNAL      Submitted (24-AUG-1999) Institut de Genetique Humaine, CNRS, UPR
            1142, rue de la Cardonille, Montpellier Cedex 5 34396, France
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source       1..487
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            /codon_start=2
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            /db_xref="GI:7211527"
            /translation="VAICNPILYPMVMSNKLSAOLLSIVYIGFLHPLVHSLRLT
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            LT"
BASE COUNT      131 a      105 c      77 g      174 t
ORIGIN
Query Match      100.0%; Score 487; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.5e-98;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ttagcgaatgtaaccccttgcttataccagtgatgagtcacaacactcagcgctca 60
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DB 1 ttagcgaatgtaaccccttgcttataccagtgatgagtcacaacactcagcgctca 60
OY 61 gtgtcgaatgtaaccccttgcttataccagtgatgagtcacaacactcagcgctca 120
    |||||||
DB 61 gtgtcgaatgtaaccccttgcttataccagtgatgagtcacaacactcagcgctca 120
OY 121 attgcgaactactctcgaaggttaacatacattcttactcgtgaaatttaca 180
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DB 121 attgcgaactactctcgaaggttaacatacattcttactcgtgaaatttaca 180
OY 181 actgttcaaatcttcgtgaatggttcacatacgaacataataattattttgg 240
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DB 181 actgttcaaatcttcgtgaatggttcacatacgaacataataattattttgg 240
OY 241 tgcctttatatacaaaatccacttgaactcaataccttatacctcgtgctctt 300
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DB 241 tgcctttatatacaaaatccacttgaactcaataccttatacctcgtgctctt 300
OY 301 tgaatctcgaaaaaaagtcgaagaaggcgaagaagccttcacatgcggcgc 360
    |||||||
DB 301 tgaatctcgaaaaaaagtcgaagaaggcgaagaagccttcacatgcggcgc 360
OY 361 ccatcgtcttctgtctcactgtactaaggaactcgaactcctcgtgagtcgtcgc 420
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DB 361 ccatcgtcttctgtctcactgtactaaggaactcgaactcctcgtgagtcgtcgc 420
OY 421 atcttgcttagctgaagacaaagatgtaattctcgttttcaacagatataatcc 480
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DB 421 atcttgcttagctgaagacaaagatgtaattctcgttttcaacagatataatcc 480
OY 481 cctgcta 487
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DB 481 cctgcta 487
    |||||||

RESULT 3
AX242110 486 bp DNA linear PAT 26-SEP-2001
LOCUS      AX242110
DEFINITION Sequence 858 from Patent WO0127158.
ACCESSION  AX242110
VERSION    AX242110.1 GI:15798985
KEYWORDS
SOURCE     synthetic construct.
ORGANISM   artificial sequence.

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REFERENCE 1 (bases 1 to 486)
 AUTHORS Bellenson, J., Smith, D., Lancel, D., Glusman, S., Fuchs, T. and Yanai, I.
 TITLE Olfactory receptor sequences
 JOURNAL Patent: WO 0127158-A 858 19-APR-2001;
 DIGISCENTS (US); YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)

FEATURES
 source 1..486
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="(H389708 nucleotide)"
 BASE COUNT 131 a 105 c 77 g 173 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 2.5e-98;
 Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 gtagccatagtaacccttcttaccagatgatagtccaaactcagcgctca 61
 Db 1 GTAGCCATATGTAATCCCTTGTTCAGATGATGTCACAAACTCAGCGCTCAG 60
 QY 62 ttgctaaagtattcatabatgtaattgtttccgtgcatccctctgttcaatgagttacta 121
 Db 61 TTGCTAAGATTTTCATATGTAATGTTCCGTTCATCTGCTCATGAGATTACGA 120
 QY 122 ttggcgaactacttctgcaggttttaacataatatttcttcttctggaatttaca 181
 Db 121 TTGGCGACTACTTCTCGAGGTTTACATTAATATTCATTTCTGTAATTTTACAA 180
 QY 182 ctgtcaaaattcagcaatggtccatctattacagcaactaaataattattttgt 241
 Db 181 CTGTCAAAATTTTCATGCAATGTCATCTATTAAAGCCTAATTAATTTTGTGT 240
 QY 242 gctttatacaaataccacttaactaactaataatctctatactcgtgtctctt 301
 Db 241 GCTTTATACAAATACCCTTAAATGATCATATCATCTTAACTGCTGCTCTTT 300
 QY 302 gatattctgaaaaaaagtcgaaaaaggcagaagaagcctctccacatgagcgcc 361
 Db 301 GATATTCTGAAAAAAGTCGAAAAAGGCGAGAAAGCCCTTCCACATCCGCGGCC 360
 QY 362 caatcgtcttctgctcattgtactacggaactctgattcttaactgattgtcctgca 421
 Db 361 CATCTGCTTCTCTCTCATTTGTAAGGAACTCTGATCTTCAATGATGCGCTCTGCA 420
 QY 422 tctgcttagctgaagaacgaagaagaagtattctctgttttacaagattaatcc 481
 Db 421 TCTGCGTTAGCTGAGACCAAGCAAGAGTGTATCTCTGTTTACAGATTATATCC 480
 QY 482 ctgcta 487
 Db 481 CTGCTA 486

RESULT 4
 AX181394 487 bp DNA linear PAT 07-AUG-2001
 LOCUS AX181394
 DEFINITION Sequence 182 from Patent WO0146262.
 ACCESSION AX181394
 VERSION AX181394.1 GI:15141512
 KEYWORDS
 SOURCE Chimpanzee.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 487)
 AUTHORS Rouquier, S. and Giorgi, D.
 TITLE Olfactory receptor genes and pseudogenes in primates and mouse
 JOURNAL Patent: WO 0146262-A 182 28-JUN-2001;
 CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
 FEATURES Location/Qualifiers

source 1..487
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /note="Taxon = 9598; gene = PTR210; Accession
 DDBJ/EMBL/GenBank = AF1797"
 CDS 1..487
 /product="Olfactory receptor"
 /protein_id="CAC50200.1"
 /db_xref="GI:15141513"
 /translation="VAICNPPLYPVMMSKLSAQLISIVYIGFLPVLVSLRLT
 FCRPNIHYCEIILOLFISGNGPSINLMITFICAFQIPIPLMTIILISYRVLEDI
 LKKSEKGRSAFSTCSAHLISVSLYGYGLIPMYVPASGLAEDBDKVSLEPTIIIP
 IL"

BASE COUNT 129 a 107 c 78 g 173 t
 ORIGIN

Query Match 98.0%; Score 477.4; DB 6; Length 487;
 Best Local Similarity 98.8%; Pred. No. 2e-96;
 Matches 481; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ttagccatagtaacccttcttaccagatgatagtccaaactcagcgctca 60
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 QY 121 attcgcaactacttctgcaggttttaacataatatttcttcttctggaatttaca 180
 Db 121 ATTGCGACTACTTCTCGAGGTTTACATTAATATTCATTTCTGTAATTTTACAA 180
 QY 181 actgttcaaaattcagcaatggtccatctattacagcaactaaataattattttg 240
 Db 181 ACTGTTCAAAATTTTCATGCAATGTCATCTATTAAAGCCTAATTAATTTTGTG 240
 QY 241 tgctttatacaaatccacttaactaactaataatctctatactcgtgtctctt 300
 Db 241 TGCTTTTATACAAATACCCTTAAATGATCATATCATCTTAACTGCTGCTCTT 300
 QY 301 tgaattctgaaaaaaagtcgaaaaaggcagaagaagcctctccacatgagcgcc 360
 Db 301 TGATATTCTGAAAAAAGTCGAAAAAGGCGAGAAAGCCCTTCCACATGCGAGCGCC 360
 QY 361 caatcgtcttctgctcattgtactacggaactctgattcttaactgattgtcctgca 420
 Db 361 CCATCTGCTTCTCTCTCATTTGTAAGGAACTCTGATCTTCAATGATGCGCTCTGCA 420
 QY 421 atctgcttagctgaagaacgaagaagaagtattctctgttttacaagattaatcc 480
 Db 421 ATCTGCGTTAGCTGAGACCAAGCAAGAGTGTATCTCTGTTTACAGATTATATCC 480
 QY 481 cctgcta 487
 Db 481 CCTGCTA 487

RESULT 5
 AF179735 487 bp DNA linear PRI 09-MAR-2000
 LOCUS AF179735
 DEFINITION Pan troglodytes olfactory receptor (PTR210) gene, partial cds.
 ACCESSION AF179735
 VERSION AF179735.1 GI:7211484
 KEYWORDS
 SOURCE Chimpanzee.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 487)
 AUTHORS Rouquier, S., Blancher, A. and Giorgi, D.
 TITLE The olfactory receptor gene repertoire in primates and mouse:

evidence for reduction of the functional fraction in primates
Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2870-2874 (2000)

JOURNAL
MEDLINE
REFERENCE
AUTHORS
JOURNAL

2 (bases 1 to 487)
Giorgi, D.G. and Rouquier, S.P.
Direct Submission
Submitted (24-AUG-1999) Institut de Genetique Humaine, CNRS, UPR
1142, rue de la Cardonille, Montpellier Cedex 5 34396, France

Location/Qualifiers

FEATURES

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/protein_id="AA040330.1"
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/translation="VAICNPPLYPMVMSNKLTAOLLSIVYIGFLPHLVHSLRLT
FCRNTHFYECILLOLEKISNGSPINAMIFEGAFIOIPIIMTIIISRYLFDI
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BASE COUNT 129 a 107 c 78 g 173 t
ORIGIN

Query Match 98.0%; Score 477.4; DB 9; Length 487;
Best Local Similarity 98.8%; Pred. No. 2e-96;

Matches 481; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY 61 gtgtcaagatattcatatgtaattgtgttccctgacccctgtgtcatgtgagttact 120
DB 61 gtgtcaagatattcatatgtaattgtgttccctgacccctgtgtcatgtgagttact 120
OY 121 attggaactaacttcctgcaggtttaacataataattcttcaattgaaatttaca 180
DB 121 attggaactaacttcctgcaggtttaacataataattcttcaattgaaatttaca 180
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DB 121 attggaactaacttcctgcaggtttaacataataattcttcaattgaaatttaca 180
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DB 301 tgaatcttgaataaaagtcgaaagggcagaagcactcttcacacatgagggcg 360
OY 361 ccattctgtctgtcctcatgtactgacgaacttgaacttcatgtaattgtgctggc 420
DB 361 ccattctgtctgtcctcatgtactgacgaacttgaacttcatgtaattgtgctggc 420
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DB 421 atctggcttaagcagaagcagaagaagtgtatctctgttttaacagattataatcc 480
OY 481 cctgcta 487
DB 481 cctgcta 487

RESULT 6
AX181383 485 bp DNA linear PAT 07-AUG-2001
LOCUS AX181383
DEFINITION Sequence 171 from Patent WO0146262.

ACCESSION AX181383
VERSION AX181383.1 GI:15132985
KEYWORDS
SOURCE

ORGANISM

Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

REFERENCE

1 (bases 1 to 485)
Rouquier, S. and Giorgi, D.
Olfactory receptor genes and pseudogenes in primates and mouse
Patent: WO 0146262-A 171 28-JUN-2001.
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES

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/db_xref="taxon:9598"
misc_feature
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DDBJ/EMBL/GenB a"

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Query Match 95.5%; Score 465; DB 6; Length 485;
Best Local Similarity 98.6%; Pred. No. 1.2e-93;

Matches 480; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

OY 1 tgaagcatalgtatcccttgcttaccagtgatgagtcgaacaaactcagcgctca 60
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DB 61 gtgtcaagatattcatatgtaattgtgttccctgacccctgtgtcatgtgagttact 120
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DB 301 tgaatcttgaataaaagtcgaaagggcagaagcactcttcacacatgagggcg 360
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DB 361 ccattctgtctgtcctcatgtactgacgaacttgaacttcatgtaattgtgctggc 420
OY 421 atctggcttaagcagaagcagaagaagtgtatctctgttttaacagattataatcc 480
DB 421 atctggcttaagcagaagcagaagaagtgtatctctgttttaacagattataatcc 480
OY 481 cctgcta 487
DB 479 cctgcta 485

RESULT 7
AF179729 485 bp DNA linear PRI 09-MAR-2000
LOCUS AF179729
DEFINITION Pan troglodytes PTR204 pseudogene, partial sequence.
ACCESSION AF179729
VERSION AF179729.1 GI:7211473
KEYWORDS
SOURCE chimpanzee.
ORGANISM Pan troglodytes

REFERENCE	Mammalia; Eutheraia; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Eumariota, Metazoa; Primates; Catarrhini; Homnidae; Pan.
TITLE	1 (bases 1 to 485)
JOURNAL	Rouquier,S., Blancher,A. and Giorgi,D. The olfactory receptor gene repertoire in primates and mouse: evidence for reduction of the functional fraction in primates Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2870-2874 (2000) 20183981
MEDLINE	2 (bases 1 to 485)
REFERENCE	Giorgi,D.G. and Rouquier,S.P. Direct Submission Submitted (24-AUG-1999) Institut de Genetique Humaine, CNRS, DPR 1142, rue de la Cardonille, Montpellier Cedex 5 34396, France
JOURNAL	location/qualifiers
AUTHORS	1..485
TITLE	/organism="Pan troglodytes"
JOURNAL	/db_xref="taxon:9598"
REFERENCE	<1..>485
MEDLINE	/gene="PTR204"
FEATURES	/pseudo
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BASE COUNT	130 a 107 c 77 g 171 t
ORIGIN	
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Oy	1 tgtaacatagtgaacccttgcttcatccagtgatgagtgcacaacctcaggcgca 60
Dd	1 tttnaccatttatgcccttcctttatccaagtagtgtgatccaaactaacggcgcta 60
Oy	61 gtgtgaagtattcatagtlaattgtgtttccctgcacccctcgtgtcatalgtgatttact 120
Dd	61 GTTGCTAAGCATTTTCATATGTAATTGGTTCCTGCATCCTCGTTGCATAGTAGTTTACT 120
Oy	121 attgcgactaatcttcgcagggtttaacaatatcatattctctactgtgaatttaca 180
Dd	121 ATTGGACATACTTCCAGGTGAACAATAATATATTCTCACTGGAAATTTTACA 180
Oy	181 actgtcaaaattcatgcgaatgagtcacatcttaagaacacataattatttttgg 240
Dd	181 ACTGTCAAAATTTATGCAATGTCGCCATCTATTAAAGCACATAATGATATTTATTTGG 240
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Dd	241 TGCCTTTAFACAAATACCACCTTAATGACGATATAATCTTTAPACGATGCTCTTT 300
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Dd	301 TGATATTTCTGAAAAAAGCTGAAAAAGGGCGAGAAGCAAAGCCTTCTCCATGACGCGC 360
Oy	361 ccactgctttctgtcctatgtactacgaacctgactctcacatgtagtgcctgc 420
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Oy	481 cctgcta 487
Dd	479 CCTGCTA 485
RESULT	8
LOCUS	AX241993 988 bp DNA linear PAT 26-SEP-2001
DEFINITION	Sequence 741 from Patent WO0127158.
ACCESSION	AX241993
VERSION	AX241993.1 GI:15798868
KEYWORDS	
SOURCE	synthetic construct.

ORGANISM	synthetic construct artificial sequence.					
REFERENCE	1 (bases 1 to 988)					
AUTHORS	Bellenson,J., Smith,D., Lancet,D., Glusman,G., Fuchs,T. and Yanai,I.					
TITLE	Olfactory receptor sequences					
JOURNAL	Patent: WO 0127158-A 741 19-APR-2001;					
FEATURES	Discents (US) ; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) Location/Qualifiers					
SOURCE	1..988 /organism="synthetic construct" /db_xref="taxon:32630" /note="(H38g590 nucleotide)"					
BASE COUNT	250 a	231 c	165 g	342 t		
ORIGIN						
Query Match	65.5%	Score 319;	DB 6;	Length 988;		
Best Local Similarity	78.4%;	Pred. No. 3.3e-61;				
Matches	382; Conservative	0;	Mismatches 105;	Indels	0;	Gaps 0;
OY	1	tgtagcatalgtgaatcccttgcttcatccagtgaatgltccaacaactcagcgctca	60			
Dd	370	tgtaccatfagtcacattcccttgctttatccagtgatgtccaatfagccctctgactca	429			
OY	61	gttgtcaaglatcttaattgtaattggtttccctgcatacccttgctcagtgaggttact	120			
Dd	430	gtttatfaggtatattcatatttatgttggttttctgcattcacgccattcatgtgggtttgt	489			
OY	121	atttgagctaactctctgcaggtttaaoataatacataattattctacttgaatttcca	180			
Dd	490	atttgattatccwtttctgcaggtccaaattattatattattttctgactgtgaattttaca	549			
OY	181	actgtccaacttcataatgatgcacatctcattaagcaactaaataattatttgg	240			
Dd	550	gctgttcacaaattttcttgccacaaatcccttagatgaattatcttgcattttcatcttttc	609			
OY	241	tgtctttatacaataaccacttlaattgactaataatcttatactcgtggtgctt	300			
Dd	610	agcattttatacaaagctttacattttatgacctgtatgcgtctactctatattctcttc	669			
OY	301	tgaattctgaaaaaaagtcgtgaagaaggcgcaagaagcctctccacatcgcgcg	360			
Dd	670	tgcacatccctgaaaagaagctcgaaagaagctgaagccttcttactgtgacgtgc	729			
OY	361	ccaatgtcttctgtcctatgttactagcgaactctgactctcatgatatgagtcctgc	420			
Dd	730	ccatttgcctctgtgctcttctttgttttacggcaccctcttcttcantgatgagttctag	789			
OY	421	atctgtcttagctgaagaccaaagaagaagtgtatctctcgttttitaacagatataatcc	480			
Dd	790	gctgtgacatcagctgcagatcagccaaatgatattctttatttaccacaaatgaattatcc	849			
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Dd	850	ttttacta 856				
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LOCUS	AC024892 Homo sapiens chromosome 3 clone RP11-214N20, WORKING DRAFT					
DEFINITION	SEQUENCE, 11 unordered pieces.					
ACCESSION	AC024892					
VERSION	AC024892.11 GI:16117893					
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.					
SOURCE	human.					
ORGANISM	Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
REFERENCE	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., 1 (bases 1 to 150083)					
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbarta,J.,					

RESULT 10
AC105564/c
LOCUS
DEFINITION
AC105564
Rattus norvegicus clone CH230-250G11, *** SEQUENCING IN PROGRESS
***, 60 unordered pieces.
AC105564
VERSION
AC105564.1 GI:18092786
KEYWORDS
HTG; HTGS_PHASE1.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 138556)
Muzny,D.M., Adams,C., Adio-Oduola,B., All-oshman,F.R., Allen,C.,
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Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Monabdt,K.,
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Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
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Weinstock,G. and Gibbs,R.
TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
TITLE
COMMENT
Unpublished
2 (bases 1 to 138556)
Direct Submission
Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GNE2
Center clone name: CH230-250G11
Summary Statistics
Assembly program: Phrap; version 0.990329first call to

findPhrapList

Consensus quality: 104982 bases at least Q40
Consensus quality: 113437 bases at least Q30
Consensus quality: 120052 bases at least Q20
Estimated insert size: 98776; sum-of-coverage estimation
Quality coverage: 0x in Q20 bases; agorose-1p estimation
Quality coverage: 1.3x in Q20 bases; sum-of-coverage estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a working draft sequence. It currently
consists of 60 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

Contig	Length	Quality	Notes
1	12026	contig of 12026 bp in length	
12027	12126	gap of unknown length	
12127	17583	contig of 5457 bp in length	
17584	17683	gap of unknown length	
17684	22927	contig of 5244 bp in length	
22928	23027	gap of unknown length	
23028	27987	contig of 4960 bp in length	
27988	28087	gap of unknown length	
28088	32504	contig of 4417 bp in length	
32505	32604	gap of unknown length	
32605	35333	contig of 2729 bp in length	
35334	35433	gap of unknown length	
35434	37327	contig of 1894 bp in length	
37328	37427	gap of unknown length	
37428	40912	contig of 3485 bp in length	
40913	41012	gap of unknown length	
41013	44129	contig of 3117 bp in length	
44130	44229	gap of unknown length	
44230	46597	contig of 2268 bp in length	
46598	46697	gap of unknown length	
46698	50418	contig of 3721 bp in length	
50419	50518	gap of unknown length	
50519	52990	contig of 2472 bp in length	
52991	53090	gap of unknown length	
53091	55622	contig of 3432 bp in length	
55623	55622	gap of unknown length	
55623	59005	contig of 2383 bp in length	
59006	59105	gap of unknown length	
59106	61667	contig of 2562 bp in length	
61668	61667	gap of unknown length	
61668	63899	contig of 2132 bp in length	
63900	63999	gap of unknown length	
64000	68087	contig of 4088 bp in length	
68088	68187	gap of unknown length	
68188	70694	contig of 2507 bp in length	
70695	70794	gap of unknown length	
70795	73386	contig of 2592 bp in length	
73387	73486	gap of unknown length	
73487	75692	contig of 2206 bp in length	
75693	75792	gap of unknown length	
75793	77929	contig of 2137 bp in length	
77930	78029	gap of unknown length	
78030	79296	contig of 1267 bp in length	
79297	79396	gap of unknown length	
79397	82238	contig of 2842 bp in length	
82239	82338	gap of unknown length	
82339	84658	contig of 2320 bp in length	
84659	84758	gap of unknown length	
84759	87336	contig of 2578 bp in length	
87337	87436	gap of unknown length	
87437	89496	contig of 2060 bp in length	
89497	89596	gap of unknown length	
89597	90917	contig of 1321 bp in length	
90918	91017	gap of unknown length	
91018	92625	contig of 1608 bp in length	

92626	92725	gap of unknown length
92726	93955	contig of 1230 bp in length
93956	94055	gap of unknown length
94056	95238	contig of 1183 bp in length
95239	95338	gap of unknown length
95339	96506	contig of 1168 bp in length
96507	96606	gap of unknown length
96607	98414	contig of 1808 bp in length
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100271	100370	gap of unknown length
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107739	109065	contig of 1327 bp in length
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112202	113509	contig of 1308 bp in length
113510	113609	gap of unknown length
113610	115100	contig of 1491 bp in length
115101	115200	gap of unknown length
115201	116535	contig of 1335 bp in length
116536	116635	gap of unknown length
116636	118099	contig of 1464 bp in length
118100	118199	gap of unknown length
118200	119225	contig of 1026 bp in length
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122557	122656	gap of unknown length
122657	124309	contig of 1653 bp in length
124310	124409	gap of unknown length
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LOCUS	AY074239	11	RESULT 11
DEFINITION	AY074239	693 bp	DNA linear ROD 04-FEB-2002
ACCESSION	Mus musculus olfactory receptor MOR182-11P pseudogene, partial sequence.		
VERSION	AY074239		
KEYWORDS	AY074239.1	GI:18481401	
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Zhang, X. and Firestein, S.		
TITLE	The olfactory receptor gene superfamily of the mouse		
JOURNAL	Nat. Neurosci. 5 (2), 124-133 (2002)		
PUBMED	11802173		
REFERENCE	2 (bases 1 to 693)		
AUTHORS	Adams, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-JAN-2002) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
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	/evidence=not_experimental		
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ORIGIN			

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Best Local Similarity	74.9%	Pred. No. 3.8e-55;		
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RESULT 12
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LOCUS Rattus norvegicus isolate HFV-FD1 olfactory receptor mRNA, partial
DEFINITION cds.
ACCESSION AF091575
VERSION AF091575.1 GI:3769640
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 663)
AUTHORS Singer,M.S., Hughes,T.E., Shepherd,G.M. and Greer,C.A.
TITLE Isolation of olfactory receptor mRNA sequences from olfactory bulb
JOURNAL glomerular layer
REFERENCE 2 (bases 1 to 663)
AUTHORS Singer,M.S., Hughes,T.E., Shepherd,G.M. and Greer,C.A.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1998) Section of Neurobiology, Yale University
School of Medicine, 236 FMB, 333 Cedar Street, New Haven, CT 06510,
USA
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IFL"
BASE COUNT 161 a 137 c 119 g 246 t
ORIGIN

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Best Local Similarity 75.0%; Pred. No. 7.9e-55;
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QY 301 tgcattatcgaataaaagctcgaagaagcgaagaagcctctccacatgcyggcgc 360
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QY 361 ccactgctctctgctcattgactacggaactctgattctatgattgctgctgc 420
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QY 481 cctgccta 484
Db 660 TCTG 663

RESULT 13
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LOCUS Mus musculus olfactory receptor MOR182-3 gene, complete cds.
DEFINITION AY073096
ACCESSION AY073096
VERSION AY073096.1 GI:18479489
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 918)
AUTHORS Zhang,X. and Firestein,S.
TITLE The olfactory receptor gene superfamily of the mouse
JOURNAL Nat. Neurosci. 5 (2), 124-133 (2002)
REFERENCE 2 (bases 1 to 918)
AUTHORS Adams,M.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2002) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
FEATURES
Source location/Qualifiers
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KEYWORDS
SOURCE
ORGANISMREFERENCE
AUTHORS

HTG: HTGS_PHASE1.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 138556)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alshrocks,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
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Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hayes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C.,
Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Licharge,O., Lien,C., Liu,J., Liu,W.,
Loulseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokwuo,S.,
Ogun,M., Okunolu,G., Oragunye,N., Ovielo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
Ruliz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N.,
Slissen,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Washington,S., Williams,G., Williamson,A., Wlarczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 138556)

Worley,K.C.

Direct Submission

Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GNE2

Center clone name: CH230-250G11

Summary Statistics

Assembly program: Phrap; version 0.990329first call to

findThrapList

Consensus quality: 104982 bases at least Q40

Consensus quality: 113437 bases at least Q30

Consensus quality: 120052 bases at least Q20

Estimated insert size: 98776; sum-of-contrigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 1.3x in Q20 bases; sum-of-contrigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 12026: contig of 12026 bp in length
12027 12126: gap of unknown length
12127 17583: contig of 5457 bp in length
17584 17683: gap of unknown length
17684 22927: contig of 5244 bp in length
22928 23027: gap of unknown length
23028 27987: contig of 4960 bp in length
27988 28087: gap of unknown length
28088 32504: contig of 4417 bp in length
32505 32604: gap of unknown length
32605 35333: contig of 2729 bp in length
35334 35433: gap of unknown length
35434 37327: contig of 1894 bp in length
37328 37427: gap of unknown length
37428 40912: contig of 3485 bp in length
40913 41012: gap of unknown length
41013 44129: contig of 3117 bp in length
44130 44229: gap of unknown length
44230 46597: contig of 2368 bp in length
46598 46698: gap of unknown length
46699 50419: contig of 3721 bp in length
50419 50518: gap of unknown length
50519 52990: contig of 2472 bp in length
52991 53090: gap of unknown length
53091 56522: contig of 3432 bp in length
56523 56622: gap of unknown length
56623 59005: contig of 2383 bp in length
59006 59105: gap of unknown length
59106 61667: contig of 2562 bp in length
61668 61767: gap of unknown length
61768 63899: contig of 2132 bp in length
63900 63999: gap of unknown length
64000 68087: contig of 4088 bp in length
68088 68187: gap of unknown length
68188 70694: contig of 2507 bp in length
70695 70794: gap of unknown length
70795 73865: contig of 2592 bp in length
73866 73867: gap of unknown length
73868 75692: contig of 2206 bp in length
75693 75792: gap of unknown length
75793 77929: contig of 2137 bp in length
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78030 79296: contig of 1267 bp in length
79297 79396: gap of unknown length
79397 82238: contig of 2842 bp in length
82239 82338: gap of unknown length
82339 84658: contig of 2320 bp in length
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84759 87336: contig of 2578 bp in length
87337 87436: gap of unknown length
87437 89496: contig of 2060 bp in length
89497 90917: contig of 1321 bp in length
90918 91017: gap of unknown length
91019 92625: contig of 1608 bp in length
92626 92725: gap of unknown length
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96607 98414: contig of 1808 bp in length
98415 98514: gap of unknown length

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* 100371 101914: contig of 1544 bp in length
* 101915 102014: gap of unknown length
* 102015 103378: contig of 1364 bp in length
* 103379 103478: gap of unknown length
* 103479 104660: contig of 1182 bp in length
* 104661 104760: gap of unknown length
* 104761 106384: contig of 1624 bp in length
* 106385 106485: gap of unknown length
* 106485 107639: contig of 1154 bp in length
* 107639 107739: gap of unknown length
* 107739 109065: contig of 1327 bp in length
* 109066 109165: gap of unknown length
* 109166 110732: contig of 1567 bp in length
* 110733 110832: gap of unknown length
* 110833 112101: contig of 1269 bp in length
* 112102 112201: gap of unknown length
* 112201 113509: contig of 1308 bp in length
* 113510 113609: gap of unknown length
* 113610 115100: contig of 1491 bp in length
* 115101 115200: gap of unknown length
* 115201 115335: contig of 1335 bp in length
* 115336 116635: gap of unknown length
* 116636 118099: contig of 1464 bp in length
* 118100 118199: gap of unknown length
* 118200 119225: contig of 1026 bp in length
* 119226 119325: gap of unknown length
* 119326 121099: contig of 1774 bp in length
* 121100 121199: gap of unknown length
* 121200 122556: contig of 1357 bp in length
* 122557 122656: gap of unknown length
* 122657 124309: contig of 1653 bp in length
* 124310 124409: gap of unknown length
* 124410 125647: contig of 1238 bp in length
* 125648 125747: gap of unknown length
* 125748 126786: contig of 1039 bp in length
* 126787 126887: gap of unknown length
* 126887 128160: contig of 1274 bp in length
* 128161 128260: gap of unknown length
* 128261 129777: contig of 1517 bp in length
* 129778 129877: gap of unknown length
* 129878 130977: contig of 1099 bp in length
* 130977 131076: gap of unknown length
* 131077 132445: contig of 1369 bp in length
* 132446 132545: gap of unknown length
* 132546 133844: contig of 1299 bp in length
* 133845 133944: gap of unknown length
* 133945 135012: contig of 1068 bp in length
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Query Match 57.9% Score 282.2; DB 2; Length 138556;
Best Local Similarity 73.7% Pred. No. 2.9e-53;
Matches 359; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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OY 1 tgaatcctgaaataaagctgaaagcgcaagcaagcctctccacatgcgcgc 60
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DB 135143 TCTAACCCATATGCAACCCCTGCTCATCTTGTGTGATGTCACAGAGTGTGCATTG 135202
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 gtgtcaagatcatatgtaattgatttcctgcacccctcgtgtcattgaatttact 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 135203 CCTGATTAAGTGTTCATATATATGCGTTTTCGATCCACTTGTTCATGTGGCATATTAT 135262
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 121 attgcgaactcttcgcaggtttaacataatatttctactctgaaattllaca 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 135263 ATTTAGACTTAACCTTGTGCAAGTCAATGTATAGATCACTTTACTGTGAGATCCTGGC 135322
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 181 actgttcaaaattcatgcaatggtccatctataacgcacctaataattattttgg 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 135323 TCTTATACAAATTTCTTGCAACGACCATCTATTATGATTCGTCGTCATTCTTTC 135382
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 241 tgccttatacaaaatcaccaacttaataactataatctcttactcgtgtcctt 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 135383 TGCCGTAATACAGGCATTACCTTCATGAGTGTGCAAGTCTCTCATGCCCATGTCTCTT 135442
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OY 301 tgaattctgaaaaaaagctgaaagcgcaagcaagcctctccacatgcgcgc 360
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DB 135443 TTCATCCCTGAAACAAAGTCTCAGAGAGTGAAGAAAAGCCTTCTCCACTGCAATGC 135502
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OY 361 ccactgcttctgtctcatgtactacggaacctgactctcatgtatgtgcctgc 420
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DB 135503 CCACCTGCTCTGCTCTCTTGTCTATGGAACCTCTTCATGTATGTGAGCCCTGG 135562
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OY 421 atctgcttagcttgaaagcaagaatgfatctctcgttttaacagattataatcc 480
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DB 135563 GTCTGACCAAGTAATATATGAATATAATGTAATCTGTTTACCCATTGTGATTC 135622
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 481 cctgccta 487
| | | | |
DB 135623 TCTACTA 135629
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Search completed: June 27, 2002, 11:17:02
Job time: 3515 sec

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RESULT	1
AAH84016	
ID	AAH84016 standard; DNA; 487 BP.
AC	AAH84016;
XX	
DT	25-SEP-2001 (first entry)
XX	
DE	Human olfactory receptor encoding gene 4.
XX	
KW	olfactory receptor; primate; mouse; human; food processing industry;
KW	aromas; perfumery; toxic substance; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200146262-A2.
PD	
PD	28-JUN-2001.
XX	
PF	22-DEC-2000; 2000WO-IBO2017.
XX	
PR	22-DEC-1999; 99US-0171746.
PR	21-DEC-2000; 2000US-0747155.
XX	
PA	(CNRS) CNRS CENT NAT RECH SCI.
XX	
PI	Rouquier S, Glorj D;
DR	WPI: 2001-381911/40.
DR	P-PSDB; AAG98521.
XX	
XT	Nucleic acids encoding primate and murine olfactory receptors, useful

PT for analysis odours e.g. in food processing and perfumery -
XX
XX
PS Claim 1: Page 273-274; 482bp; English.

CC The invention relates to olfactory receptors (AG98432-AG98609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours).
XX
XX

Sequence 487 BP; 131 A; 105 C; 77 G; 174 T; 0 other;

Query Match 100.0%; Score 487; DB 22; Length 487;
Best Local Similarity 100.0%; Pred. No. 5e-116;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tgaagcacaatgtaacccctgcttatacagatgatagtgccaacaaactcagcgctca 60
DB 1 tgaagcacaatgtaacccctgcttatacagatgatagtgccaacaaactcagcgctca 60
QY 61 gtgtgaatgatttataatgtaattgttctctgcatcctctggttcacatgtaagttact 120
DB 61 gtgtgaatgatttataatgtaattgttctctgcatcctctggttcacatgtaagttact 120
QY 121 atcggaactaactctctgaggtttaacataataattcttactgtaagttacta 180
DB 121 atcggaactaactctctgaggtttaacataataattcttactgtaagttacta 180
QY 181 actgttcaaaattcaatgaaatgtaacatcatttaacgacataataattattttgg 240
DB 181 actgttcaaaattcaatgaaatgtaacatcatttaacgacataataattattttgg 240
QY 241 tgcctttacaaataccacttaagtactatcattacttacttactcgtgctctt 300
DB 241 tgcctttacaaataccacttaagtactatcattacttacttactcgtgctctt 300
QY 301 tgaattctgaaaaaaagctcgaagaaggcgaagaagcctctccacatgagcgac 360
DB 301 tgaattctgaaaaaaagctcgaagaaggcgaagaagcctctccacatgagcgac 360
QY 361 ccattctgcttctgtctcaatgtactacggaactctgactcattcattgtaatgctctgc 420
DB 361 ccattctgcttctgtctcaatgtactacggaactctgactcattcattgtaatgctctgc 420
QY 421 atctggttagctgaagcgaagaagatgactctcgttttaacagatatatttc 480
DB 421 atctggttagctgaagcgaagaagatgactctcgttttaacagatatatttc 480
QY 481 cctgcta 487
DB 481 cctgcta 487

RESULT 2
AAH32285
ID AAH32285 standard; DNA; 486 BP.

XX
XX
AC AAH32285;
XX
XX 30-JUL-2001 (first entry)

DE Human olfactory receptor polynucleotide, seq ID NO: 858.

XX
XX
KW Human: olfactory receptor. OR: primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation; ds.

XX
XX
OS Homo sapiens.
XX
XX MO200127158-A2.

XX
PD 19-APR-2001.

PF 06-OCT-2000; 2000MO-US27582.

XX 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

XX (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI: 2001-290713/30.

XX
XX
PS Claim 8; page 523; 1857bp; English.

CC The present sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,
CC and can be used for determining differences in the olfactory faculties
CC of different individuals.
XX
XX

Sequence 486 BP; 131 A; 105 C; 77 G; 173 T; 0 other;

Query Match 99.8%; Score 486; DB 22; Length 486;
Best Local Similarity 100.0%; Pred. No. 9.1e-116;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 gtagcacaatgtaacccctgcttatacagatgatagtgccaacaaactcagcgctcag 61
DB 1 gtagcacaatgtaacccctgcttatacagatgatagtgccaacaaactcagcgctcag 60
QY 62 ttgcaaatgattcattatgtaattgttctcgcacatcctctggttcacatgtaagttacta 121
DB 62 ttgcaaatgattcattatgtaattgttctcgcacatcctctggttcacatgtaagttacta 120
QY 122 ttgcaactaacttctgaggtttaacataataattcttactgtaagttacta 181
DB 122 ttgcaactaacttctgaggtttaacataataattcttactgtaagttacta 180
QY 182 ctgttcaaaattcattcaatgtaatgctcattcaacgacataataattattttgt 241
DB 182 ctgttcaaaattcattcaatgtaatgctcattcaacgacataataattattttgt 240
QY 242 gctttatacaaaatccacttaagtactatcaactccttatacccggtgtctt 301
DB 242 gctttatacaaaatccacttaagtactatcaactccttatacccggtgtctt 300
QY 302 gataattcgaaaaaaaagctcgaagaaggcgaagaagcctctccacatgagcgac 361
DB 302 gataattcgaaaaaaaagctcgaagaaggcgaagaagcctctccacatgagcgac 360
QY 361 catctgcttctgtctcaatgtactacggaactctgactcattcattgtaatgctctgc 421
DB 361 catctgcttctgtctcaatgtactacggaactctgactcattcattgtaatgctctgc 420
QY 422 tctggttagctgaagcgaagaagatgactctcgttttaacagatatatttc 481
DB 422 tctggttagctgaagcgaagaagatgactctcgttttaacagatatatttc 480

OY 482 ctgccta 487
|||||
DB 481 ctgccta 486

RESULT 3

AAH83992
ID AAH83992 standard; DNA; 487 BP.

AC AAH83992;

XX 25-SEP-2001 (first entry)

DE Hylobates lar olfactory receptor encoding gene 4.

KW Olfactory receptor; primate; mouse; human; food processing industry;
KM aromas; perfumery; toxic substance; ds.

XX Hylobates lar.

XX WO200146262-A2.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-IB02017.

XX 22-DEC-1999; 99US-0171746.
PR 21-DEC-2000; 2000US-0747155.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Rouquier S, Giorgi D;

XX WPI: 2001-381911/40.

XX P-PSDB; AAG98506.

PT Nucleic acids encoding primate and murine olfactory receptors, useful
for analysis odours e.g. in food processing and perfumery -

PS Claim 1; Page 238; 482pp; English.

CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours).

SQ Sequence 487 BP; 129 A; 107 C; 78 G; 173 T; 0 other;

Query Match 98.0%; Score 477.4; DB 22; Length 487;

Best Local Similarity 98.8%; Pred. No. 1.5e-113;
Matches 481; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 tgaaccataatgtaaccccttgcttattccagtgtatggtccaaacaaactagcgctca 60
DB 1 tgaaccataatgtaaccccttgcttattccagtgtatggtccaaacaaactagcgctca 60
OY 61 gtggttaagtattatgataatggttctctgcacccctcgtgtcatgtgagtttact 120
DB 61 gtggttaagtattatgataatggttctctgcacccctcgtgtcatgtgagtttact 120
OY 121 attgagactactctctgcaggtttaacataacattattctactgtgaaatttaca 180
DB 121 attgagactactctctgcaggtttaacataacattattctactgtgaaatttaca 180
OY 181 actgtcaaaattatgacgaatggtccatctataacgacacaaataattatttttg 240
DB 181 actgtcaaaattatgacgaatggtccatctataacgacacaaataattatttttg 240

OY 241 tgcattatacaaatccccacttaatgactatcatatctcttactcgtgtcctt 300
DB 241 tgcattatacaaatccccacttaatgactatcatatctcttactcgtgtcctt 300
OY 301 tgaattctgaaaaaaagctgaaaggcgaaagcaagccttcacatgcgcg 360
DB 301 tgaattctgaaaaaaagctgaaaggcgaaagcaagccttcacatgcgcg 360
OY 361 ccactcgtcttctgtctactgtactacggaactcgtacatcgtatgtgcttcgc 420
DB 361 ccactcgtcttctgtctactgtactacggaactcgtacatcgtatgtgcttcgc 420
OY 421 atctgcttagctgaaagacacaaagtatattctcgttttacaagatataatcc 480
DB 421 atctgcttagctgaaagacacaaagtatattctcgttttacaagatataatcc 480
OY 481 cctgccta 487
DB 481 cctgccta 487

RESULT 4

AAH83986
ID AAH83986 standard; DNA; 485 BP.

AC AAH83986;

XX 25-SEP-2001 (first entry)

DE Pan troglodytes olfactory receptor encoding gene 10.

KW Olfactory receptor; primate; mouse; human; food processing industry;
KM aromas; perfumery; toxic substance; ds.

XX Pan troglodytes.

XX WO200146262-A2.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-IB02017.

XX 22-DEC-1999; 99US-0171746.
PR 21-DEC-2000; 2000US-0747155.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Rouquier S, Giorgi D;

XX WPI: 2001-381911/40.

XX P-PSDB; AAG98501.

PT Nucleic acids encoding primate and murine olfactory receptors, useful
for analysis odours e.g. in food processing and perfumery -

PS Claim 1; Page 227; 482pp; English.

CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours).

SQ Sequence 485 BP; 130 A; 107 C; 77 G; 171 T; 0 other;

Query Match 95.5%; Score 465; DB 22; Length 485;

Best Local Similarity 98.6%; Pred. No. 2.3e-110;
Matches 480; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

OY 1 tgaaccataatgtaaccccttgcttattccagtgtatggtccaaacaaactagcgctca 60

Db 1 tgcagccataatcccttgccttaccagtgatgctccaaacacagcgctca 60
QY 61 gtctgaagatataatgaatgttccctgcacccctgcgttgcgttact 120
Db 61 gtctgaagatataatgaatgttccctgcacccctgcgttgcgttact 120
QY 121 atcgcgaactctcgcaggttaacataacatattctactgtgaattaca 180
Db 121 atcgcgaactctcgcaggttaacataacatattctactgtgaattaca 180
QY 181 acitctcaaatctcagatgttccatctataacgcataataatttttgg 240
Db 181 acitctcaaatctcagatgttccatctataacgcataataatttttgg 240
QY 241 tgccttatacaaatccacttaataatgactatctctatctgtgctct 300
Db 241 tgccttatacaaatccacttaataatgactatctctatctgtgctct 300
QY 301 tgatactcgaataaagctgaagaaggcagaagaagcctctccacatgcgcgc 360
Db 301 tgatactcgaataaagctgaagaaggcagaagaagcctctccacatgcgcgc 360
QY 361 ccactcgtctctctcctcctcctcctcctcctcctcctcctcctcctc 420
Db 361 ccactcgtctctcctcctcctcctcctcctcctcctcctcctcctcctc 420
QY 421 atcgcgttagctgaagaacgaagaagtgatctcctgttccacgataatcc 480
Db 421 atcgcgttagctgaagaacgaagaagtgatctcctgttccacgataatcc 480
QY 481 cctgccta 487
Db 479 cctgccta 485

RESULT 5
AAH32168
ID AAH32168 standard; DNA; 988 BP.
AC AAH32168;
DT 30-JUL-2001 (first entry)
DE Human olfactory receptor polynucleotide, SEQ ID NO: 741.
XX Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation; ds.
OS Homo sapiens.
PN WC00127158-A2.
PD 19-APR-2001.
PE 06-OCT-2000; 2000MO-US27582.
XX 08-OCT-1999; 990S-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX (DIGT-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
DR New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX Claim 8; Page 478; 1857bp; English.

CC The present sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,
CC and can be used for determining differences in the olfactory faculties
CC of different individuals.
XX
SQ Sequence 988 BP; 250 A; 231 C; 165 G; 342 T; 0 other;

Query Match 65.5%; Score 319; DB 22; Length 988;
Best Local Similarity 78.4%; Pred. No. 1.1e-72;
Matches 382; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1 tgcagccataatcccttgccttaccagtgatgctccaaacacagcgctca 60
Db 370 tgcagccataatcccttgccttaccagtgatgctccaaacacagcgctca 429
QY 61 gtctgaagatataatgaatgttccctgcacccctgcgttgcgttact 120
Db 430 gtctgaagatataatgaatgttccctgcacccctgcgttgcgttact 489
QY 121 atcgcgaactctcgcaggttaacataacatattctactgtgaattaca 180
Db 490 atcgcgaactctcgcaggttaacataacatattctactgtgaattaca 549
QY 181 acitctcaaatctcagatgttccatctataacgcataataatttttgg 240
Db 181 acitctcaaatctcagatgttccatctataacgcataataatttttgg 240
QY 241 tgccttatacaaatccacttaataatgactatctctatctgtgctct 300
Db 550 tgccttatacaaatccacttaataatgactatctctatctgtgctct 609
QY 301 tgatactcgaataaagctgaagaaggcagaagaagcctctccacatgcgcgc 360
Db 670 tgatactcgaataaagctgaagaaggcagaagaagcctctccacatgcgcgc 729
QY 361 ccactcgtctctcctcctcctcctcctcctcctcctcctcctcctcctc 420
Db 730 ccactcgtctcctcctcctcctcctcctcctcctcctcctcctcctc 789
QY 421 atcgcgttagctgaagaacgaagaagtgatctcctgttccacgataatcc 480
Db 790 atcgcgttagctgaagaacgaagaagtgatctcctgttccacgataatcc 849
QY 481 cctgccta 487
Db 850 ttcacta 856

RESULT 6
AAI99556
ID AAI99556 standard; cDNA; 953 BP.
AC AAI99556;
DT 04-JAN-2002 (first entry)
DE Human expressed polynucleotide SEQ ID NO 19.
XX Human; neotropic; neuroprotective; cytosolic; dermatological; virologic;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischistosomal; antianemic; antidiabetic; cancer;
KW antirheumatic; hepatotropic; cerebrotropic; anti-inflammatory;

KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
SS.
XX Homo sapiens.
XX WO200155387-A1.
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01310.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225478.
PR 14-AUG-2000; 2000US-0225479.
PR 14-AUG-2000; 2000US-0225480.
PR 14-AUG-2000; 2000US-0225481.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.

DB 181 atgttaacgatttcctgactgaccctctataatttttaagtctttatttctc 240
QY 241 tgccttaatacaaatccacccttaattgactatcatacttctatctgtgacct 300
DB 241 tggcttaatacaaggtactctacttctgctctgtctctatgacatttgcctct 300
QY 301 tgaattctgaaaaaaagctgaaaaaggcagaagcaccctctccacatgcgcgc 360
DB 301 tacaattcaaaaaaaagcagtcacaaagcacaagaagcctctccacatgcgcgc 360
QY 361 ccactgctctctgtctcattgactaaggaactctgacttcaatgattgctgcgc 420
DB 361 ccactctctctcgtctgattactaagcctctctctctcaatgattgctgcgcgc 420
QY 421 atctgcttagctggaagcacaagaagctattctctgttttaaccgattataatcc 480
DB 421 atctcacaagcagatgataagaatagatgtagatgatttcaactgcatcattcc 480
QY 481 cctgcta 487
DB 481 ttctcta 487

RESULT 8
AAH31676
ID AAH31676 standard; DNA; 942 BP.
XX AAH31676;
AC
XX
XX 30-JUL-2001 (first entry)
DE Human olfactory receptor polynucleotide, SEQ ID NO: 249.
XX
XX
XX Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation; ds.
XX
OS Homo sapiens.
XX
XX WO200127158-A2.
PN
XX
XX 19-APR-2001.
PD
XX 06-OCT-2000; 2000MO-US27582.
PF
XX
XX 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
XX (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
PI
XX
XX WPI: 2001-290713/30.
DR
XX
XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
XX
PS Claim 8; Page 276-277; 1857pp; English.

The present sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,
CC and can be used for determining differences in the olfactory faculties

CC of different individuals.
XX
SQ Sequence 942 BP; 255 A; 196 C; 152 G; 339 T; 0 other;
Matches 334; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

Query Match 49.7%; Score 242.2; DB 22; Length 942;
Best Local Similarity 68.6%; Pred. No. 6,6e-53;
Matches 334; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 1 tgaagcattatgtaaccctgcttaccagtgatgatagtcacaactcagcgtca 60
DB 384 tgaagcattatgtaaccctgcttaccagtgatgatagtcacaactcagcgtca 443
QY 61 gttgtaagtaattcattgtaattgtgttccctgctcctggttgaattgattct 120
DB 444 gctgtgctctccattttagtggtgctctcccaagccttaattcaatgaagctctat 503
QY 121 atgcgaactaacttctgcaggttaacataatacatattctactctggaatttaca 180
DB 504 atcagatttaacctctgcgaattctcaacataatacatattctactctggaatttaca 563
QY 181 actgtcaaaaattcattgcaatggtcactatataacgcaactaataatttttgg 240
DB 564 actgttatagtattccctgactgacccctctattatttcttaattggttttatttgc 623
QY 241 tgccttaatacaaatccacccttaattgactatcataatctcttaactggtgcctt 300
DB 624 tggctcaattcgaattcaccatttgcacagttcttaattcttaacatttgcctttt 683
QY 301 tgaattctgaaaaaaagctgaaaaaggcagaagcaccctctccacatgcgcgc 360
DB 684 cacactctcaaaaaaagagctgtttagagcgtagaagaagccttccaccttgcgcgc 743
QY 361 ccactgctctctgtctcattgactaaggaactctgacttcaatgattgctgcgc 420
DB 744 ccactctctctgtctcattgactaaggaactctgacttcaatgattgctgcgcgc 803
QY 421 atctgcttagctggaagcacaagaagctattctctgttttaaccgattataatcc 480
DB 804 atctcacaagcagatgataagaatagatgtagactctgtcttataacataatcc 863
QY 481 cctgcta 487
DB 864 ttgctca 870

RESULT 9
AAS42326
ID AAS42326 standard; cDNA; 945 BP.
XX AAS42326;
AC
XX
XX 18-DEC-2001 (first entry)
DE Human cDNA encoding olfactory receptor AORL127.
XX
XX
XX Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
KW ss; food additive; cosmetic; fragrance; pharmaceutical additive.
XX
XX
OS Homo sapiens.
XX
XX
XX WO200168805-A2.
PN
XX
XX 20-SEP-2001.
PD
XX
XX 13-MAR-2001; 2001MO-US07771.
PF
XX
XX
PR 13-MAR-2000; 2000US-0188914.
PR 24-MAR-2000; 2000US-0192033.
PR 12-APR-2000; 2000US-0198474.
PR 24-APR-2000; 2000US-0199335.
PR 26-MAY-2000; 2000US-0207702.
PR 23-JUN-2000; 2000US-0213849.

PR 16-AUG-2000; 2000US-0226534.
PR 07-SEP-2000; 2000US-0230732.
PR 07-FEB-2001; 2001US-0266862.

XX
XX
XX (SENO-) SENOMYX INC.

XX
XX
XX Zozulya S;

DR WPI; 2001-570867/64.
DR P-PSDB; AAU24633.

XX
XX
XX Nucleic acids encoding human olfactory G protein-coupled receptors,
PT useful for screening for compounds involved in olfactory sensation,
PT where the compounds can be used in the food, pharmaceutical and
PT cosmetic industries to customise odours -

XX
XX
XX Claim 1; Page 136; 319pp; English.

XX
XX
XX The invention relates to nucleic acids encoding human olfactory
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
CC specifically recognise molecules, odourants, that elicit specific
CC olfactory sensation. The human olfactory receptors and polynucleotides
CC encoding them are useful for screening a library of chemical compounds
CC for compounds that are useful for screening a library of chemical compounds
CC their activity are useful for pharmacological and genetic modulation of
CC olfactory signalling pathways. Therefore, they can be used in the food,
CC pharmaceutical and cosmetic industries to customise odours and
CC fragrances. The present sequence encodes a human olfactory receptor of
CC the invention.

XX
XX
XX Sequence 945 BP; 256 A; 196 C; 153 G; 340 T; 0 other;

Query Match 49.7%; Score 242.2; DB 22; Length 945;
Best Local Similarity 68.6%; Pred. No. 6.6e-53;
Matches 334; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

OY 1 ttagcacaatgtaaccccttcttaccagtgatgagtcacaacacagcgctca 60
DB 384 ttagcacaatgtaaccccttcttaccagtgatgagtcacaacacagcgctca 443
OY 61 gtgtgcaagatcttcataatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
DB 444 gctgtgcaagatcttcataatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 503
OY 121 attgcgactaacttctcgaagtttaacataatatttctactgtgaatttaca 180
DB 504 attgcgactaacttctcgaagtttaacataatatttctactgtgaatttaca 563
OY 181 actgttcaaatattcgaatgagtcacatctataacgacacataatatttttg 240
DB 564 actgttcaaatattcgaatgagtcacatctataacgacacataatatttttg 623
OY 241 tgccttatacaaatcccaacttaagtactacataatccttcaactcgtgtctt 300
DB 624 tgccttatacaaatcccaacttaagtactacataatccttcaactcgtgtctt 683
OY 301 tgaatctcgaataaaagtcgaagagcgaagcaagccttcacacatgacgagc 360
DB 684 caaatcccaataaaagtcgaagagcgaagcaagccttcacacatgacgagc 743
OY 361 ccaatcgtcttctgtcactgtactaaggaactcgtacatcgaatgagtcgctc 420
DB 744 ccaatcgtcttctgtcactgtactaaggaactcgtacatcgaatgagtcgctc 803
OY 421 accttgctagctgaagacacagaatgfatctcgtgttttcaagatataatcc 480
DB 804 accttgctagctgaagacacagaatgfatctcgtgttttcaagatataatcc 863
OY 481 ccttgcta 487
DB 864 ttgtcta 870

RESULT 10
AAH31707
ID AAH31707 standard; DNA; 958 BP.

XX
XX
XX AAH31707;

XX
XX
XX 30-JUL-2001 (first entry)

DE Human olfactory receptor polynucleotide, SEQ ID NO: 280.

XX
XX
XX Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation; ds.

XX
XX
XX Homo sapiens.

XX
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XX WO200127158-A2.

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XX 19-APR-2001.

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XX 06-OCT-2000; 2000WO-US27582.

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XX 08-OCT-1999; 99US-0158615.

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XX 24-FEB-2000; 2000US-0184809.

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XX (DIGI-) DIGISCENTS.

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XX (YEDA) YEDA RES & DEV CO LTD.

XX
XX
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

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XX WPI; 2001-290713/30.

XX
XX
XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -

XX
XX
XX Claim 8; Page 289-290; 1857pp; English.

XX
XX
XX The present sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,
CC and can be used for determining differences in the olfactory faculties
CC of different individuals.

XX
XX
XX Sequence 958 BP; 261 A; 200 C; 150 G; 347 T; 0 other;

Query Match 48.5%; Score 236; DB 22; Length 958;
Best Local Similarity 69.1%; Pred. No. 2.6e-51;
Matches 337; Conservative 0; Mismatches 150; Indels 1; Gaps 1;

OY 1 ttagcacaatgtaaccccttcttaccagtgatgagtcacaacacagcgctca 60
DB 369 ttagcacaatgtaaccccttcttaccagtgatgagtcacaacacagcgctca 428
OY 61 gtgtgcaagatcttcataatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
DB 429 gctatagccttgatcattatagtggtgtgtgtgtgtgtgtgtgtgtgtgtgt 488
OY 121 attgcgactaacttctcgaagtttaacataatatttctactgtgaatttaca 180
DB 489 attgcgactaacttctcgaagtttaacataatatttctactgtgaatttaca 548
OY 181 actgttcaaatattcgaatgagtcacatctataacgacacataatatttttg 240

Db 549 atgttaagaatttccttactgagcccttatttaatttttaagctttatttttc 608
Qy 241 tgcctttatacaataccacttaatactatactatacttactcgtgtctctt 300
Db 609 tgttcaataaaggatcatcatttttactgttcttcttctatacatgttctctt 668
Qy 301 tgaatc-tctgaataaagaagctgaagaaggaagccttcccaatgagcgc 359
Db 669 tacaatcttaaaaaaagctgcgaagaacataagaagccttcccaatgtgag 728
Qy 360 cccatctgtcttcgtcctatgtactgaacgtatcttcaatgatagtgctctg 419
Db 729 cccatcttctatcgttcttatactatggtccctctctcttcaatgatagtgacccctg 788
Qy 420 catctggttagctgaagcaagaagaagtgtatctcgtctttacagattaatc 479
Db 789 catctccacaagcagatgatcaagatggtgagctcttatttaacactgcatattc 848
Qy 480 cccgtcta 487
Db 849 ctctccta 856

RESULT 11

AAH31705

ID AAH31705 standard; DNA; 972 BP.

AC AAH31705;

D7 30-JUL-2001 (first entry)

DE Human olfactory receptor polynucleotide, SEQ ID NO: 278.

KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation; ds.

OS Homo sapiens.

PN WO200127158-A2.

PD 19-APR-2001.

PE 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
PS Claim 8; Page 288-289; 1857pp; English.

CC The present sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,

CC and can be used for determining differences in the olfactory faculties
CC of different individuals.

SQ Sequence 972 BP; 269 A; 203 C; 151 G; 349 T; 0 other;

Query Match

47.1%; Score 229.4; DB 22; Length 972;

Best Local Similarity 66.9%; Pred. No. 1.3e-49;

Matches 326; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

Qy 1 tgaagcaatgtaatcccttgccttatacagtgatgtaagtcacaaactcagcgctca 60
Db 369 tgaagcaatgtaatcccttgccttatacagtgatgtaagtcacaaactcagcgctca 428
Qy 61 gtgtcaagatattcaatgtaattgtttccctgcatacctctgtgtcatgagttact 120
Db 429 gctattagctgtgcatattatagtggtccttcttcatgtcttaacatgaaattttt 488
Qy 121 attggaactaacttctgcaaggtttaacataatataattttcttactgtgaatttaca 180
Db 489 attcagattaaaccttctgtaattccacataacataacacactttcctgagacattatcc 548
Qy 181 actgtcaaaatttcaatgcatgcatctatacgaactaataatatttttgg 240
Db 549 atgttaagaatttccttactgactgtattcttatacttaacttcaatgattttatttcgc 608
Qy 241 tgcctttatacaataccacttaatactatactatacttactcgtgtctctt 300
Db 609 agattcaattcaagttttacacattggaactatttatactatacactgttctct 668
Qy 301 tgaatc-tctgaataaagaagctgaagaaggaagccttcccaatgagcgc 360
Db 669 tacaatcttaaaaaaagctgcgaagaacataagaagccttcccaatgtgagc 728
Qy 361 cccatctgtcttcgtcctatgtactgaacgtatcttcaatgatagtgctctgc 420
Db 729 tcatcttactatgtaatttatactatggtcccttgccttcaatgatagtggtcctgc 788
Qy 421 atctggttagctgaagcaagaagaagtgtatctcgtctttacagattaatc 480
Db 789 atccccgaagcagatgacgaagatgagtgctcttatttaacactgcatcgtcttc 848
Qy 481 cctgcta 487
Db 849 tttaatta 855

RESULT 12

AAH31701

ID AAH31701 standard; DNA; 927 BP.

AC AAH31701;

D7 30-JUL-2001 (first entry)

DE Human olfactory receptor polynucleotide, SEQ ID NO: 274.

KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation; ds.

OS Homo sapiens.

PN WO200127158-A2.

PD 19-APR-2001.

PE 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -

XX Claim 8; Page 287; 1857p; English.

XX The present sequence is one of a number of isolated polynucleotides
XX which encode polypeptides involved in olfactory sensation. The
XX polynucleotides can be used in screening for olfactory agonists and
XX antagonists. The methods allow for the determination of primary
XX scents and the identification of the odour receptors used to detect
XX these primary scents. The methods also enable determination of
XX secondary scents and the identification of combinations of odour
XX receptors that are involved in detecting such secondary scents.
XX This enables the construction of a scent representation (also called
XX a scent fingerprint or scent profile), which may be used to re-create
XX and edit scents. Libraries of olfactory receptors are useful for
XX determining the interaction pattern of a composition with the receptors,
XX and can be used for determining differences in the olfactory faculties
XX of different individuals.

SQ Sequence 927 BP; 256 A; 203 C; 143 G; 325 T; 0 other;

Query Match 46.1%; Score 224.6; DB 22; Length 927;

Best Local Similarity 66.3%; Pred. No. 2.2e-48; Matches 323; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

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DB 369 tgaagcattatgtaacccctgtcttaccagatgatgtccacaacacgagctca 428
QY 61 gtgcctaatgattcatatgtaattgtcttcgcgacccctcgttcaatgtgattact 120
DB 429 gctattagctctgcatattatagtgagcctctcctcaagcttaacatcaagcttttc 488
QY 121 attgcgactaactcttcgaggttttaacataactattcttactcgtgaatttaca 180
DB 489 attcagatttaacccctcgttaattccacaataaacaacttcttactgagcaattacc 548
QY 181 actgtcaaaattcatgacatgtgcacatcatataacgcacataataattttttg 240
DB 549 attgttaaaagattccctgacttgcattccctattacttaacttaagtgttttttcgc 608
QY 241 tgccttatacaaaataccacatttaactgaactataactcttatactcgtgtgctct 300
DB 609 aggtctcgttcaagattttacacttggaactattcttatactatacaattaccccttc 668
QY 301 tgaatttcgaaagaaagctgaagaaagcgaagcgaagccttcacacatgcgcgc 360
DB 669 tacaacctagaagaaagcctacacaaaggagatacgaagagcgtcccccgtggggc 728
QY 361 ccaatgccttcctgctcattgatacgaagaaactgatactatgataatgtgcctcgc 420
DB 729 tcaatcctatcctgatacttatacactatgcccctcactcacttaataatctggcctgc 788
QY 421 attgccttagctgaagcacaagaagtgtatctcgttttttaacagataattcc 480
DB 789 attcgcgaagcagatgaccaaagatagatgagctctctatttaacactgcataagttcc 848
QY 481 cctgccta 487
DB 849 ttatata 855

RESULT 13
AAS42325
ID AAS42325 standard; CDNA: 978 BP.

XX AAS42325;
AC 18-DEC-2001 (first entry)
DT 18-DEC-2001 (first entry)
XX

DE Human cDNA encoding olfactory receptor AORFR126.

KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
KW ss; food additive; cosmetic; fragrance; pharmaceutical additive.

OS Homo sapiens.

PN WO200168805-A2.

PD 20-SEP-2001.

PF 13-MAR-2001; 2001MO-US07771.

PR 13-MAR-2000; 2000US-0188914.

PR 24-MAR-2000; 2000US-0192033.

PR 12-APR-2000; 2000US-0198474.

PR 24-APR-2000; 2000US-0199335.

PR 26-MAY-2000; 2000US-0207702.

PR 23-JUN-2000; 2000US-0213849.

PR 16-AUG-2000; 2000US-0226534.

PR 07-SEP-2000; 2000US-0230732.

PR 07-FEB-2001; 2001US-0266862.

PA (SENO-) SENOMYX INC.

PI Zozulya S;

DR WPI: 2001-570867/64.

XX P-PSDB; AAU24632.

XX Nucleic acids encoding human olfactory G protein-coupled receptors,
XX useful for screening for compounds involved in olfactory sensation,
XX where the compounds can be used in the food, pharmaceutical and
XX cosmetic industries to customise odours -

PS Claim 1; Page 136; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory
XX receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
XX specifically recognise molecules, odourants, that elicit specific
XX olfactory sensation. The human olfactory receptors and polynucleotides
XX encoding them are useful for screening a library of chemical compounds
XX for compounds that are involved in olfactory sensation. Modulators of
XX their activity are useful for pharmacological and genetic modulation of
XX olfactory signalling pathways. Therefore, they can be used in the food,
XX pharmaceutical and cosmetic industries to customise odours and
XX fragrances. The present sequence encodes a human olfactory receptor of
XX the invention.

SQ Sequence 978 BP; 267 A; 212 C; 155 G; 344 T; 0 other;

Query Match 46.1%; Score 224.6; DB 22; Length 978;

Best Local Similarity 66.3%; Pred. No. 2.3e-48; Matches 323; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 1 tgaagcattatgtaacccctgtcttaccagatgatgtccacaacacgagctca 60
DB 417 tgaagcattatgtaacccctgtcttaccagatgatgtccacaacacgagctca 476
QY 61 gtgcctaatgattcatatgtaattgtcttcgcgacccctcgttcaatgtgattact 120
DB 477 gctattagctctgcatattatagtgagcctctcctcaagcttaacatcaagcttttc 536
QY 121 attgcgactaactcttcgaggttttaacataactattcttactcgtgaatttaca 180
DB 537 attcagatttaacccctcgttaattccacaataaacaacacttattactgagactattccc 596

PA (DIGI-) DIGISCENTS.
PA (VEDA) VEDA RES & DEV CO LTD.

XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

XX MPI; 2001-290713/30.

DR New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX

PS Claim 8; Page 285; 1857pp; English.

CC The present sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,
CC and can be used for determining differences in the olfactory faculties
CC of different individuals.
XX

SQ Sequence 944 BP; 262 A; 184 C; 152 G; 346 T; 0 other;

Query Match 43.2%; Score 210.2; DB 22; Length 944;
Best Local Similarity 64.5%; Pred. No. 1.1e-44;
Matches 314; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 1 ttgaagcacaatgaaccccttgcttaccagatgacgaacacaaactcagcgctca 60
DB 376 tgcagacacatgcaaaaccttacttaccagatcattacgaacaaactgacatcgc 435
QY 61 gttgctaagatctcacaatgcaatggttcttcctgcacacctcgtgacatgagttact 120
DB 436 gctattgctctgctcattctcagtgcttcttcacatgcttaccatgaagttctt 495
QY 121 atggagcacaacttctgcaagttacacataacatttctactgtgaatttaca 180
DB 496 atcagaccacaacctctcgaaccacacagacacacacatttctactgacattacc 555
QY 181 actgttcaaaatctcagcaatgctcaccatctaacgacataatatttttg 240
DB 556 attgttaaaagattctcagtcacgattctgtatataatttcaatgtttttttctc 615
QY 241 tgcctttatacaaaatcccaacttaagtacatcataatccttactcgtgtcctt 300
DB 616 aggttcaaatcaagtttcaacattggaattgttttgatcatatgttttctctt 675
QY 301 tgatattcgaaaaaaagctgaaagggcaagcaagccttctcacatgcggcg 360
DB 676 tacaaccttaaaaagagcttaacaaagacaaaggaagccttccacacctgtgagac 735
QY 361 ccactcgtcttctgctcattgtaacagacacacacacacacacacacacacacac 420
DB 736 ccattacataactctctcttattgtatgctcctctctctcactcactgatagtggccctgc 795
QY 421 atctgcttagctgaagacacaaagtgatctcgttttacacgatatataatcc 480
DB 796 agctcacacagacagataacagatagtatgagatatactattaccatcatatgtgcg 855
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DB 856 ttgtgta 862

Job time: 3746 sec

Thu Jun 27 14:54:41 2002

us-09-747-155-224.rng

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 27, 2002, 10:18:27 ; Search time 43.34 Seconds
(without alignments)
2760.118 Million cell updates/sec

Title: US-09-747-155-224

Perfect score: 487

Sequence: 1 tggagccatgtatccct.....cgatataatccctcgcta 487

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_patents_NA.*
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/Backfile1.seq.*

SUMMARIES

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2	103	21.1	1713	3	US-08-467-947A-1
3	93.2	19.1	1290	2	US-08-827-291A-1
4	90.8	18.6	966	3	US-08-748-506-8
5	88.4	18.2	966	3	US-08-748-506-6
6	85.2	17.3	966	3	US-08-748-506-5
7	84.4	17.3	900	4	US-09-085-371-5
8	73.2	15.0	966	3	US-08-748-506-7
9	71.6	14.7	984	3	US-08-748-506-9
10	51.4	10.6	1320	1	US-08-599-252-84
11	51.4	10.6	1320	1	US-08-436-074-57
12	51.4	10.6	1320	5	PCT-US96-06352-84
13	51.4	10.6	1320	5	PCT-US96-06583-84
14	45.4	9.3	7218	1	US-08-232-463-14
15	38.4	7.9	2251	4	US-08-991-677-11
16	37.2	7.6	2429	4	US-09-386-493-3
17	34.6	7.1	236	2	US-08-744-905A-1
18	34.6	7.1	1241	1	US-07-593-657-6
19	34.6	7.1	1241	4	US-08-942-012B-3
20	34.4	7.1	6243	2	US-09-056-075-1
21	34	7.0	1828	2	US-08-988-876-2
22	33.4	6.9	10968	2	US-08-680-327-2
23	33.4	6.9	10968	4	US-09-228-246-1
24	32.8	6.7	246240	2	US-08-724-394A-20
25	32.8	6.7	246240	2	US-08-724-394A-21
26	32.8	6.7	246240	2	US-08-724-394A-22
27	32.6	6.7	565	2	US-08-731-722-7

28	32.6	6.7	934	2	US-08-731-722-6	Sequence 6, Appli
29	32.6	6.7	934	2	US-08-731-722-6	Sequence 6, Appli
30	32.6	6.7	1183	2	US-08-731-722-8	Sequence 8, Appli
31	32.6	6.7	1183	2	US-08-731-722-5	Sequence 8, Appli
32	32.6	6.7	1186	2	US-08-731-722-5	Sequence 5, Appli
33	32.6	6.7	1186	2	US-08-731-722-5	Sequence 5, Appli
34	32.6	6.7	1218	2	US-08-731-722-4	Sequence 4, Appli
35	32.6	6.7	1218	2	US-08-731-722-4	Sequence 4, Appli
36	32.6	6.7	3926	2	US-08-731-722-1	Sequence 1, Appli
37	32.6	6.7	3926	2	US-08-731-722-1	Sequence 1, Appli
38	32.6	6.7	3926	2	US-08-731-722-2	Sequence 2, Appli
39	32.6	6.7	3926	2	US-08-731-722-2	Sequence 2, Appli
40	32.6	6.7	3933	2	US-08-731-722-3	Sequence 3, Appli
41	32.6	6.7	3933	2	US-08-731-722-3	Sequence 3, Appli
42	32.4	6.7	15766	4	US-09-338-907-73	Sequence 73, Appli
43	32.4	6.7	15766	4	US-09-218-207-73	Sequence 73, Appli
44	32.4	6.7	37950	4	US-09-338-907-183	Sequence 183, App
45	32.4	6.7	37950	4	US-09-218-207-183	Sequence 183, App

ALIGNMENTS

RESULT 1
US-08-467-948A-1
Sequence 1, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 116..1003
US-08-467-948A-1

Query Match 21.1%; Score 103; DB 2; Length 1713;
Best Local Similarity 51.4%; Pred. No. 5.5e-20;
Matches 238; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

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DB 494 GTGGCATTGCGCCACCTCTCCGATATTTCATCATGACCTGGAAAGTGTGACACT 553
QY 62 ttgctaaagtattcaatgttaattggtttccctgcatccctgtgtcatgtgttacta 121
DB 554 CTGGGCAATCACTTCTCGAATGTGGCTCCCTCGGTATGATGATGATGATGATGATG 613
QY 122 ttggaactaactcttcgaagtttaacataatacatatttctctgtgaatttcaaa 181
DB 614 CTAAAGACTGCGCTTTTGTGGCTCTGTAATCAACCACTTCTTGTGAATCTGTCT 673
QY 182 ctgttcaaaatlcatgtcaatgtgtcactataacgaactaataataatttttgt 241
DB 674 GTCTCTAGGCTGGCTGTGCTGATACCTGGCTCAACGAGTGATCTTTGAAGCTGCG 733
QY 242 gctttatacaataaccacttaatagtactataatcttataactgtgtgtcttt 301
DB 734 ATGTTCAATCTGTGGGACCACTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 793
QY 302 gatacttgaaaaaaagcttgaagaaggaagcaagcaagcctctcacaatgtgagcgc 361
DB 794 GGCATCTGTAGGATCCAGTCTGGGAGGCGCGCAAGAGGCTTCTCACCCTGCTCC 853
QY 362 catctgtcttctgtcatgttactaagaaactgtactatgtatgtgtgtgtgtgtgt 421
DB 854 CACCTGTGCGTAGGAGACTCTTCTTTGGSAGCGCCATGCGTATGATGATGATGATG 913
QY 422 tctgtgcttgaagcaagcaagcaagcaagcaagcaagcaagcaagcaagcaagca 464
DB 914 TCCCGCATCTCTGAG 956

RESULT 2

US-08-467-947A-1
Sequence 1, Application US/08467947A

Patent No. 6090575

GENERAL INFORMATION:

APPLICANT: LI, YI

APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN

APPLICANT: GENTZ, REINER

APPLICANT: BULT, CAROL J.

APPLICANT: SUTTON III, GRANGER G.

APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS: Coupled Receptor GPR1

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467, 947A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 116..1003
US-08-467-947A-1

Query Match 21.1%; Score 103; DB 3; Length 1713;
Best Local Similarity 51.4%; Pred. No. 5.5e-20;
Matches 238; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 2 gtagcatalgtatcccttgcttataccagtgatgtcccaaaactcaagcgtcag 61
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DB 554 CTGGGCAATCACTTCTCGAATGTGGCTCCCTCGGTATGATGATGATGATGATGATG 613
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DB 794 GGCATCTGTAGGATCCAGTCTGGGAGGCGCGCAAGAGGCTTCTCACCCTGCTCC 853
QY 362 catctgtcttctgtcatgttactaagaaactgtactatgtatgtgtgtgtgtgtgt 421
DB 854 CACCTGTGCGTAGGAGACTCTTCTTTGGSAGCGCCATGCGTATGATGATGATGATG 913
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DB 914 TCCCGCATCTCTGAG 956

RESULT 3

US-08-827-291A-1
Sequence 1, Application US/08827291A

Patent No. 5874243

GENERAL INFORMATION:

APPLICANT: Macina, Roberto

APPLICANT: Sathe, Ganesh

TITLE OF INVENTION: NOVEL OLRG15 RECEPTOR

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA


```

? COUNTRY:
? ZIP: 19406
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/827,291A
? FILING DATE: 28-MAR-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: King, William T
? REGISTRATION NUMBER: 30,954
? REFERENCE/DOCKET NUMBER: GP50001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610-270-5015
? TELEFAX: 610-270-5090
?
? TELEX:
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1290 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? US-08-827-291A-1

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Query Match          19.1%; Score 93.2; DB 2; Length 1290;
Best Local Similarity 49.6%; Pred. No. 2.8e-17;
Matches 239; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

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QY 5 gccatatgtaacccctgcttaccagtgatgagtcacaaacctcaagcgcagttg 64
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 668 GCCATTGGCCACCCTTAAGATACCAATCTCATGAGCCCTAAATTGGGACTATG 727
QY 65 ctaagattcataatgtaattggttccctgcatcctcgtgttcacgtgagttacttg 124
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 728 ACTGCTTTTCGTCGATCGCGGCTCTACAGATGATTCATTTCGTAGCCACATTT 787
QY 125 cgactaaccttcgcaggtttaaataatacatatttctacgtggaatttacaactg 184
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 788 TCCTTCCTACTGCTGGTCTCGGGAATAGCCCATCTTCTGTGAGTTACCTTCCCTA 847
QY 185 ttcaaatctcagcaatggtgcacatctatcaacgcactaataattattttgtgct 244
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 848 CTAATCTCTCATGCAATGACACATCAATTTGAAAGTTATTTCATTTGCTCTATA 907
QY 245 ttatacaaatccactttaatgactataataatctctatactcgtgtgctcttgat 304
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 908 GTAATGCTGTTTCCCTGTGCAATCATCATTCCTTCATGCTGGAGTTATTCGCT 967
QY 305 attctgaaaaaaagtcgaaagcgacgaagcaaacgcttctccacatgcgcgccat 364
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 968 GTATTTCACATGGGATGGAGAGGTCGTGCAAAAGCTTTCACGACCTGTTCTCTCAC 1027
QY 365 ctgcttctctctcactgtaacgaactgacttcaatgtaagtgtgctcgcactc 424
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1028 CTGATGCTGGTGGAAATGCTTAAGAGCAAGTTGTTTCATGTCATACAGCCCATCT 1087
QY 425 ggctttagctgaagcaagaacaaagtlatctcctglttttacaagattataatccctg 484
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1088 GATGCTCTCCCAAGCAGACAGCAAGCTGTGTGTATTTACACACATCCTACTCCCATG 1147
QY 485 ct 486
   ||
Db 1148 CT 1149

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RESULT 4
US-08-748-506-8
? Sequence 8, Application US/08748506
? Patent No. 6159707
? GENERAL INFORMATION:
? APPLICANT: Ronnett et al.
? TITLE OF INVENTION: NOVEL SPERM RECEPTORS
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Leydig, Volt & Mayer, Ltd.
? STREET: Two Prudential Plaza, Suite 4900
? CITY: Chicago
? STATE: IL
? COUNTRY: US
? ZIP: 60601-6780
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/748,506
? FILING DATE: 08-NOV-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/033,751
? FILING DATE: 09-NOV-1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? REFERENCE/DOCKET NUMBER: 74940
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5600
? TELEFAX: 312-616-5700
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 966 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? US-08-748-506-8

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Query Match          18.6%; Score 90.8; DB 3; Length 966;
Best Local Similarity 49.2%; Pred. No. 1.2e-16;
Matches 239; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

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QY 1 tgtagcatatgtaatcccttgcttaccagtgatgagtcacaaacctcaagcgcac 60
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 TATGGCTATATGTTCCCACTCCACTATGCAACCCGAATGAGTGTAGTATGTGCCCA 446
QY 61 gtgtcagaatttcacatgtaattggttccctgcatcctcgtgttcagtgtgacttact 120
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 447 CTTGGCAATGTTTTCATGGGATGGATGATGATGATGATGATGATGATGATGATGAT 506
QY 121 attcgactaaccttcgcaggtttaaataatacatatttctcactggtgaatttaca 180
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 507 TTTTCTCTTGAATCTGTGTGACCCCTGTGAGATGAGACCACTTCTTGTGATCTTCACC 566
QY 181 actgtcaaaattccatgcaatggtgcacatctatcaacgcactaataattattttg 240
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 567 TCTCTGCGACTTTCCTGCTGTGTATACATCCCAATTTGAGGCTCCCATCTTTGGTAGT 626
QY 241 tgccttatacaaatccactttaatgactataataatccttatactcgtgtgctct 300
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 627 TGTCTCTGCAATATCTAGCCCTTTTTCGTGATCATTTTATCTTATGCAGAATTTCTGT 686
QY 301 tgatatctgaaaaaaagtcgaaagcgacgaagcaaacgcttccacatgcgcgc 360
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 687 TGCAGTCTGGTGTGCTTACCTTGAGGGGCGCACAAAGCCCTTTCACACTTTCCTC 746
QY 361 ccactcgttctctcactgtaacgaactcgtacttcaatgtaagtgtgctcgcgc 420
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 747 CCACCTACTGTAGTACACCTCTTTATGCTCAGAGTCTGTACTATTGAGGCTTAA 806
Oy 421 atctgcttagctgaagacacaaagtgtatctctgtttacagataatcc 480
Db 807 GTCTACCACTACACGAGATGACAAACTCTTGCCCTCTTACACACAGACTGACATC 866
Oy 481 cctgct 486
Db 867 CATGTT 872

RESULT 5
US-08-748-506-6
; Sequence 6, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnelt et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5700
; TELEFAX: 312-616-5600
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-748-506-6

Query Match 18.2%; Score 88.4; DB 3; Length 966;
Best Local Similarity 48.8%; Pred. No. 5.7e-16;
Matches 236; Conservative 0; Mismatches 248; Indels 0; Gaps 0;

Db 3 tagcctatgtaatacctcgtcttaccagtgatgtatgcaacaacacagcgctcagt 62
Oy 389 TGGGCAATATGCTCCCACTCCACTATGCAACCCGAAATGAGTGTGATGAGCCATT 448
Db 63 tgcctaatctcataatgtaattgtttccctgcatccctctgtgttcaatgagttactat 122
Oy 449 TGGCAATTTGTTTCATGCGGGAATGCGATGATAGTCTGGGACACGACCAATTATTT 508
Db 123 tgcgactaactcttcgcaaggttaacataatacatattcttactcgtgaatttacaac 182
Oy 509 NCTCTTGAACCTTGTGTGAGCTTGTGAGATAGACCACTTCTTGTGACCTTCCACCTC 568
Db 183 tgttcaaaatcagcaatgagtcataatcattaaagcacaataataattattttggg 242
Oy 569 TCCTGCACTCTGTGTGTGATACATCCCAAAACGAGGCTGCCATCTTTGTGGACGAA 628

Oy 243 ctltatacaaatlaccacttaactatcataatccttatactcgtgtgctcttg 302
Db 629 TCCTGTAATACCTACTCATTTTGTGATCCTTTATTTCTATATGACAAATTCGTGG 688
Oy 303 atattctgaaaaaagctcgaagggcagaagcaagcctcttcacatgcgagccc 362
Db 689 CAGTGTGTGTGATGCTTACCTTACCTGAGGGGCCATTAAGCTCTTTCACACTGTCTCAC 748
Oy 363 atctgcttctgtcctatctgtactacggaactctgatactctcatgtaatgagtcgctgcat 422
Db 749 ACCTACTTGTAGTACACACTTTTATGCTCTGTGCTTCTTACCTATTGAGGCCCAAT 808
Oy 423 ctggtcttagctgaagacacaaagtgtatctctgtttacagataatccccc 482
Db 809 CTAGCCACTACACGAGATGACAAACTCTTGCCCTCTTCTACACAGAGTACATCCA 868
Oy 483 tgcct 486
Db 869 TGCT 872

RESULT 6
US-08-748-506-5
; Sequence 5, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnelt et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5700
; TELEFAX: 312-616-5600
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-748-506-5

Query Match 17.5%; Score 85.2; DB 3; Length 966;
Best Local Similarity 48.3%; Pred. No. 4.5e-15;
Matches 234; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

Db 3 tagcctatgtaatacctcgtcttaccagtgatgtatgcaacaacacagcgctcagt 62
Oy 389 TGGCAATATGCTCCCACTCCACTATGCAACCCGAAATGAGTGTGATGAGCCATT 448

[illegible]

```

RESULT 7
US-09-085-371-5
: Sequence 5, Application US/09085371
: Patent No. 6218358
: GENERAL INFORMATION:
: APPLICANT: Firestein, Stuart
: APPLICANT: Zhao, Haiping
: TITLE OF INVENTION: Functional Expression of, and Assay for, Functional Cellular Re
: TITLE OF INVENTION: Vivo
: FILE REFERENCE: P0151IUS2 / 09805059
: CURRENT APPLICATION NUMBER: US/09/085,371
: CURRENT FILING DATE: 1998-05-19
: PRIOR APPLICATION NUMBER: US 08/891,243
: PRIOR FILING DATE: 1997-07-10
: PRIOR APPLICATION NUMBER: US 60/045,961
: PRIOR FILING DATE: 1997-05-07
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 5
: LENGTH: 900
: TYPE: DNA
: ORGANISM: Rat
US-09-085-371-5

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Query Match	17.38;	Score 84.4;	DB 4;	Length 900;
Best Local Similarity	48.48;	Pred. No. 7.4e-15;		
Matches 235; Conservative	0;	Mismatches 251;	Indels 0;	Gaps 0;

Oy 1 tggagcctaagatnatacccttgctttatccagtgatgatgtccacaacatcagcgctca 60
 Db 384 tgggctatccgtatccacacccactaccccgctatgtcagaacccgatagtgtgca 443
 Oy 61 gtctctaagatattcatgatgaattggtttccgcacccctgttcatagttggttact 120
 Db 444 gatggcaccgtgataccctggcggttgtaggttttgybatccatggttaagaatttccctaa 503
 Oy 121 attggaactaactcttcgcaggttgtaacataacatactattctactggtgaatttaca 180
 Db 504 ttctccgcgtcttaccgtgtgcgcccaacacataacacactttctccgtgagtgtctcc 563

Oy	181	acgttcaaaatcatatgcacatgtgtccatcttaacagcactaaatatttttttgg	240
Db	544	attgtccaacctgtcatatgcactgtgcacatgtccacagcagagcttaacagactttctctggc	623
Oy	241	tgctttatacaatacccatcttaatgaatcatatatactctatatactgtgtgcctt	300
Db	624	cattttttttctgtctgggaccgcctctctgttaccctgtgggcacatccacatgycacataag	683
Oy	301	tgaatatctgaaaaaaagtcctgaaaaagggcagaagaacgcttctccacatgycggcgc	360
Db	684	tgcgtgtgtgycacatccctcagctgtctgctggccgcacataagcctttcaacactgtgctc	743
Oy	361	ccaatctgcttctctgtcattgttaactacagaactctgaatcttaatgtaatgtgtgcctgc	420
Db	744	caacctcaactgtgtgacatcatctctatgcagccagatattcatatcatgtccagcgctaa	803
Oy	421	atctgctctagctgaagcccaagcaagaatgtattctctgttttaacaggtttaatcttc	480
Db	804	ggcactctcaagcttttgacacacaacaagcttgcctctgttaactacagctgcatatgacc	863
Oy	481	ccctgct 486	
Db	864	gtttgtt 869	

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1      RESULT 8
2      US-08-748-506-7
3      Sequence 7, Application US/08/748506
4      Patent No. 6159707
5      GENERAL INFORMATION:
6      APPLICANT: Ronnelt et al.
7      TITLE OF INVENTION: NOVEL SPERM RECEPTORS
8      NUMBER OF SEQUENCES: 31
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: Leydig, Volt & Mayer, Ltd.
11     STREET: Two Prudential Plaza, Suite 4900
12     CITY: Chicago
13     STATE: IL
14     COUNTRY: US
15     ZIP: 60601-6780
16     COMPUTER READABLE FORM:
17     MEDIUM TYPE: Floppy disk
18     COMPUTER: IBM PC compatible
19     OPERATING SYSTEM: PC-DOS/MS-DOS
20     SOFTWARE: PatentIn Release #1.0, Version #1.25
21     CURRENT APPLICATION DATA:
22     APPLICATION NUMBER: US/08/748,506
23     FILING DATE: 08-NOV-1996
24     CLASSIFICATION: 435
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER: US 60/033,751
27     FILING DATE: 09-NOV-1995
28     CLASSIFICATION: 435
29     ATTORNEY/AGENT INFORMATION:
30     REFERENCE/DOCKET NUMBER: 74940
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: 312-616-5600
33     TELEFAX: 312-616-5700
34     INFORMATION FOR SEQ ID NO: 7:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 966 base pairs
37     TYPE: nucleic acid
38     STRANDEDNESS: double
39     TOPOLOGY: linear
40     MOLECULE TYPE: DNA (genomic)
41     US-08-748-506-7

```

Query Match	15.08;	Score 73.2;	DB 3;	Length 966;
Best Local Similarity	46.98;	Pred. No. 1.1e-11;		
Matches 228;	Conservative 0;	Mismatches 258;	Indels 0;	Gaps 0;

Oy	1	tgagccatgataatcccttgctttccagtgatgattccaaacaactaagcgctca	60
Db	387	TATGGCTATATGTTCCCACTCCACTATGCACACCCGATGAGTGTGGGTATGTGCTTA	4486
Oy	61	gttcgaagatattcataatgtaattgglltccctgcacccctctggttcattgagttact	120
Db	447	TTTGGCAATTTGTCATATGGGTGATGGATGCATGTAGTGTGGGACAGACCAATTTTAT	5066
Oy	121	atggcgaactaactcttcgcaggtttaaacaataatcattattcttaactgtaaatltaca	1806
Db	507	TTTCTCTTGAACTTCTGTGGACCCCTGTGAGATGACCACTTCTTGTGAACCTTCCACC	5666
Oy	181	actgttcaaaatttcattgcgaatggltccatctatcaacgcacaaataattatttttg	2406
Db	567	TCTCTGGCACTTGCCTGTGTGTATACATCCCAAAATGAGGCTGCCACTTTTGTGGACG	6266
Oy	241	tgcatttatacaatbaccaccttaatgaactacataatcctcthaactcgtgtgcctt	3006
Db	627	AGTGTCTGCATATTTATGTCATTTTACTGATATATTTCTTCCATCTGCAGAAATTCGT	6866
Oy	301	tgaattcttgaaaaaaagtcgtgaaggcgagaagaagccctccacatgagcgcg	3606
Db	667	TGCACTGCTGTGATGCTTACTGTAGGGGCGCCATTAAGCTTCTCTACCTGTTGATC	7466
Oy	361	ccattcgtcttcgttctcatgttactacggaactcgtactctcaatgtatgtgcgtcgc	4206
Db	747	TCACCTACTTGTAGTGCACACTCTCTATGAGCTCAACATCTGCCACTATTTGAGGTCAA	8066
Oy	421	atctgcgcttagcttgaagaacaaagaagtgatctctgttttaacggttatattcc	4806
Db	807	GTTACGACCACTCCACGAGGTGACAAACTCTTGCGCCCTCTTCTATACATCAGTGCATC	8666
Oy	481	actgct 486	
Db	867	CATGCT 872	
RESULT 9			
US-08-748-506-9			
Sequence 9, Application US/08748506			
Patent NO. 6159707			
GENERAL INFORMATION:			
APPLICANT: Ronnett et al.			
TITLE OF INVENTION: NOVEL SPERM RECEPTORS			
NUMBER OF SEQUENCES: 31			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Leydig, Volt & Mayer, Ltd.			
STREET: Two Prudential Plaza, Suite 4900			
CITY: Chicago			
STATE: IL			
COUNTRY: US			
ZIP: 60601-6780			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/748,506			
FILING DATE: 08-NOV-1996			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 60/033,751			
FILING DATE: 09-NOV-1995			
CLASSIFICATION: 435			
ATTORNEY/AGENT INFORMATION:			
REFERENCE/DOCKET NUMBER: 74940			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 312-616-5600			
TELEFAX: 312-616-5700			
INFORMATION FOR SEQ ID NO: 9:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 984 base pairs			

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;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;      MOLECULE TYPE: DNA (genomic)
US-08-748-506-9

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Query Match	14.7%	Score 71.6;	DB 3;	Length 984;
Best Local Similarity	46.7%;	Pred. No. 3.1e-11;		
Matches 227;	Conservative 0;	Mismatches 259;	Indels 0;	Gaps 0;

Oy	1	tgtagccatgataatcccttggcttctccagtgatgatgtcccaacaactcagcgctca	60
Db	387	TCCTGGCATTCTGCAAACTCCTACATTATTCACACCATATATAGAGGCCAAGATGTGCTTCCT	446
Oy	61	gttgctaaagtatttcataatgtaattggtttccctgacatccctcggttcaatgtgaattact	120
Db	447	TCTCTTTCCTCTGTTTATTTTGGGGCTTCCTTCATGAGCCAGTCCACTGTGTGATGCT	506
Oy	121	attgagactaactcttcgcaggtttcaacataatcatattctcaactggaatttaca	180
Db	507	TTCCAAAGACATTTTACTGTGTGTCCAAACATTTATTCCTCACTTTTCTGTATTTTGGACC	566
Oy	181	acgtgtccaatatctcatgcaatggttcacatcbatbaacgcataataattatcttgg	240
Db	567	ACTGGCAATTCCTCCCTGTTTCAGAAACAGAGTCATTGAGATGGCTGTTTTCACCTTGC	626
Oy	241	tgcttttatacaaatlaaccacttaatgaactataatctctaatcctgtgtgcctt	300
Db	627	TGTATTTGTGCTTTTGTGCTTCCTTCTTATAGGCATCTTTTGCAATACGCAATATAGTACT	686
Oy	301	tgatattctgaaaaaaagtcctgaaaaaggcagaagaacaaagccttccaatgycggcgc	360
Db	687	CACCATATGTGAGCTCCCTTCAGCCAGGAGCGCACAGAGAGCTTTTCCACCTGCTCCTC	746
Oy	361	ccaatctgtcttcgttcacatctgtactacgcgaacctcgaatcttaatgaatgtgctcctgc	420
Db	747	TCAATCTATTGTCTCTCTCTCTAATGTATGGCAGCTGTGTCATTTATATACCTGGAAGCAAA	806
Oy	421	atcttgctttagctgaaagaccagaagaagtatattctctgttlttacaagatataatcc	480
Db	807	GCAGAGAAGCAGACTGTGACACCAACAGAGAGGCTGCTTGTGAACATGCTGTGTGACACC	866
Oy	481	ccctgct 486	
Db	867	cccttct 872	

10
 US-08-599-252-84/C
 Sequence 84, Application US/08599252
 Patent No. 5705343
 GENERAL INFORMATION:
 APPLICANT: DRAVNA, DENNIS T.
 APPLICANT: FEDER, JOHN N.
 APPLICANT: GRIKKE, ANDREAS
 APPLICANT: KIMMEL, BRUCE E.
 APPLICANT: THOMAS, WINSTON J.
 APPLICANT: WOLFF, ROGER K.
 TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
 TITLE OF INVENTION: HEMOCHROMATOSIS
 NUMBER OF SEQUENCES: 124
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 City: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,252
FILING DATE: 09-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-599-252-84

Query Match 10.6%; Score 51.4; DB 1; Length 1320;
Best Local Similarity 61.7%; Pred. No. 1.7e-05;
Matches 82; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 349 cacatgagggcccatcgtcttctgtctatgtactaaggaaatgtaattctgttttaac 408
DB 1320 CACTTGCAGCTCGCATCAATTTGTTGTCTCTCTATGTAATCATATACATGTA 1261

QY 409 tgtgcgtccatcgtgcttagctgaagaccagaagtgtatctctgttttaac 468
DB 1260 CCTCCAGCAGCAATACTTATTCACAGACGACGCAAGTTTCTTACCTTTTCTACAC 1201

QY 469 gattataatccc 481
DB 1200 AATTGTCACTCC 1188

RESULT 11
US-08-436-074-57/c
Sequence 57, Application US/08436074
Patent No. 5753438
GENERAL INFORMATION:
APPLICANT: DRAYNA, DENNIS T.
APPLICANT: FEDER, JOHN N.
APPLICANT: GNIKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFE, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,074
FILING DATE: 08-MAY-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-074-57

Query Match 10.6%; Score 51.4; DB 1; Length 1320;
Best Local Similarity 61.7%; Pred. No. 1.7e-05;
Matches 82; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 349 cacatgagggcccatcgtcttctgtctatgtactaaggaaatgtaattctgttttaac 408
DB 1320 CACTTGCAGCTCGCATCAATTTGTTGTCTCTCTATGTAATCATATACATGTA 1261

QY 409 tgtgcgtccatcgtgcttagctgaagaccagaagtgtatctctgttttaac 468
DB 1260 CCTCCAGCAGCAATACTTATTCACAGACGACGCAAGTTTCTTACCTTTTCTACAC 1201

QY 469 gattataatccc 481
DB 1200 AATTGTCACTCC 1188

RESULT 12
PCT-US96-06352-84/c
Sequence 84, Application PC/TUS9606352
GENERAL INFORMATION:
APPLICANT: DRAYNA, DENNIS T.
APPLICANT: FEDER, JOHN N.
APPLICANT: GNIKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFE, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06352
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,252
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US96-06352-84

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Query Match	10.6%;	Score 51.4;	DB 5;	Length 1320;
Best Local Similarity	61.7%;	Pred. No. 1.7e-05;		
Matches 82; Conservative	0;	Mismatches 51;	Indels 0;	Gaps 0;

[illegible]

RESULT 13
PCT-US96-06583-84/c

Sequence 84, Application PC/TUS9606583
GENERAL INFORMATION:
APPLICANT: DRAVNA, DENNIS T.
APPLICANT: FEDER, JOHN N.
APPLICANT: GRIKKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
TITLE OF INVENTION: HEMOCHROMATOSIS
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:

Query Match 10.6%; Score 51.4; DB 5; Length 1320;

Best Local Similarity	61.78;	Pred. NO. 1.7e-05;							
Matches	82;	Conservative	0;	Mismatches	51;	Indels	0;	Gaps	0;

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Db	1320	CACCTTCGAGCTCGCATCTAATTTTGTGTCTCTCTTCTTATGGTACATCATATTCATATGTA	1261
QY	409	tgtgcgcctgcacatctgagcttagcgaagcaagaacagtgatcttcctgttttcac	468
Db	1260	CGTCCAGCCACAGCAATATCTTATTTCCAGGACACGAGGCAAGTTCTTACCCCTTTTCTACAC	1201
QY	469	gattataattccc	481
Db	1200	AATTGTCACTCCC	1188

RESULT 14
US-08-232-463-14

Sequence 14, Application US/08322463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOXP2 VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA

Oy 52 cagcgctcagttgctaagtatttcataatgtaaatgttcttgacacctggttcattg 111
||| | ||| |: : : : : : : : :
Db 1046 CAGGTCGAGGACCTTGCATYYYYYYYYYYYYYYYYYYYYYYYYYYY 1105

```
OY 112 gagttactatcgactactctcaggttacaatacattatctactcgtga 171
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1106 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1165
OY 172 aatttacaactgttcaaatlcatgcaatggtlccatctatacgcactaataat 231
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1166 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1225
OY 232 tatlttggtcttatacaaatcccaacttaagactatacatctctactcg 291
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1226 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1285
OY 292 tctgctcttgatctcgaataaaagtcctgaaagggcagaagcaagccttcac 351
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1286 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1345
OY 352 atcgagcgccatctctctctcgtcactatgactacgaaactctgactcatglat 411
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1346 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy 1405
OY 412 ggcgtcgtcatctgctgctgaagacgaagaaagtgatctctgttctac 466
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1406 yyyyyyyyyyyyyyyyyyyyyyyyyyygtaaccaaatctctatctcttaac 1460
```

RESULT 15

```
US-08-991-677-11/c
; Sequence 11, Application US/08991677A
; Patent No. 6252135
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent L
; APPLICANT: Caraway, Daniel T
; APPLICANT: Smeltzer, Richard H
; TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
; FILE REFERENCE: 50617
; CURRENT APPLICATION NUMBER: US/08/991,677A
; CURRENT FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: US 60/033,381
; EARLIER FILING DATE: 1996-12-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2251
; TYPE: DNA
; ORGANISM: Pinus taeda
US-08-991-677-11
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```
Query Match 7.9%; Score 38.4; DB 4; Length 2251;
Best Local Similarity 49.5%; Pred. No. 0.094;
Matches 99; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

OY 118 acatcgcaactactctcaggttacaatacattctactcgtgaattt 177
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 889 AATATTGGATTTGACTTCAAAAGTTATTAATTAATTAATTTTCTAAATT 830
OY 178 acaactgttcaaatlcatgcaatggtlccatctatacgaactaataattt 237
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 829 TAACCTAAATATAGATTAATTTACCAACAATTTTAAATAATAGTTAATTA 770
OY 238 tgggtcttatacaatacccaacttaagactatacatctctactcgtgtgc 297
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 769 TTTTAAATTTTGAATTTTACTTAATTTAACAAACAATTTTATCAATTAAT 710
OY 298 cttgatattcgaataaaa 317
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 709 TTTTGTATTCAAAATTA 690
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Search completed: June 27, 2002, 11:17:06
Job time: 3519 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 27, 2002, 10:18:27 ; Search time 1614.01 Seconds

(Without alignments)
4072.476 Million cell updates/sec

Title: US-09-747-155-224

Perfect score: 487

Sequence: 1 tgcatacatgtatccct.....cgatataatccctgcta 487

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gq_est1:*
10: gq_est2:*
11: gq_hlc:*
12: gq_gss:*
13: em_gss_hum:*
14: em_gss_iny:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228.2	46.9	757	12	BH278852 CH230-108
2	177.4	36.4	623	12	AZ641407 IM0503K20
3	171.2	35.2	496	12	AZ366926 IM0116D24
4	165.2	33.9	681	12	AG136576 Pan trogl
5	160.8	33.0	570	12	AZ090010 RPCI-23-4
6	150.8	31.0	404	12	AZ880560 RPCI-23-1
7	141.8	29.1	629	12	AZ019257 RPCI-23-2
8	138.2	28.4	550	12	AQ984439 RPCI-23-3
9	129.8	26.7	556	12	AZ714202 RPCI-24-8
10	129.2	26.5	649	12	BH342817 CH230-64F
11	126.8	26.0	763	12	BH109232 RPCI-24-3
12	126	25.9	611	12	AZ103967 RPCI-23-3
13	124.4	25.5	507	12	AZ560017 RPCI-23-2
14	124.4	25.5	628	12	AZ086388 RPCI-23-2
15	118.2	24.3	740	12	AZ607393 IM0429N15
16	115	23.6	508	12	AZ373636 IM0126C20
17	112.4	23.1	682	12	AZ334227 IM0065H01

18	111.6	22.9	2021	11	BC016940
19	110.8	22.8	610	12	AZ392378
20	110	22.6	642	12	AZ969227
21	109.8	22.5	656	12	BH078380
22	106.2	21.8	580	12	AZ418115
23	106	21.8	676	12	AG069165
24	105.2	21.6	646	12	AZ638594
25	102.6	21.1	675	12	AZ430777
26	101	20.7	587	12	AZ614107
27	100.2	20.6	438	12	AQ984812
28	99.4	20.4	578	12	AZ252633
29	98.2	20.4	652	12	AZ972672
30	98.2	20.2	732	10	BG068751
31	97.2	20.0	686	12	AZ086625
32	95.6	19.6	513	12	AZ082239
33	95.4	19.6	726	12	AZ255734
34	95.2	19.5	678	12	BH067899
35	94	19.3	515	12	AZ593814
36	94	19.3	580	12	AZ593814
37	93.8	19.3	711	12	BH291047
38	93.6	19.2	647	12	AZ386019
39	93.4	19.2	294	12	AQ027654
40	93.4	19.2	543	12	AZ742029
41	93.2	19.1	236	12	BH405788
42	92.8	19.1	1394	11	AK017036
43	92.8	19.1	3063	11	AK016560
44	92.6	19.0	639	12	BH078443
45	92.4	19.0	698	12	BH069789

ALIGNMENTS

RESULT 1
BH278852/c
LOCUS
DEFINITION BH278852 CH230-108016, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH278852
VERSION BH278852.1 GI:17191254
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 757)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn

A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de

Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcorI segment

Unpublished (1999)
Other:GSS: CH230-108016.TJ

Contact: Shaying Zhao
Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200
Fax: 301 838 0208

Email: szhaob@tigr.org
Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@tigr.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or_ering/information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 108 row: 0 column: 16

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..757

/organism="Rattus norvegicus"

/strain="BN/SMNH/MCW"

	LOCUS	AZ366926/c	496 bp	DNA	linear	GSS 02-Oct-2000
	DEFINITION	IM01ID24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0116D24 F, DNA sequence.				
	ACCESSION	AZ366926				
	VERSION	AZ366926.1	GI:10480626			
	KEYWORDS	GSS.				
	SOURCE	house mouse.				
	ORGANISM	Mus musculus				
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	AUTHORS	1 (bases 1 to 496) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
	TITLE	Unpublished (2000)				
	JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177				
	COMMENT	Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0116 row: D column: 24 Seq primer: CGTGTAAACAGACGGCCAGT Class: plasmid ends High quality sequence stop: 496.				
FEATURES	Location/Qualifiers					
SOURCE	1..496					
	/organism="Mus musculus"					
	/strain="C57BL/6J"					
	/db_xref="taxon:10090"					
	/clone="UUGC1M0116D24"					
	/clone_lib="Mouse 10kb plasmid UUGC1M library"					
	/sex="Male"					
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"					
	/note="Vector: PMD42nv; Purified genomic DNA from T1-musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gII473211419blAFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."					
BASE COUNT	171 a 80 c 110 g 135 t					
ORIGIN						
Query Match	35.2%; Score 171.2; DB 12; Length 496;					
Best Local Similarity	71.7%; Pred. No. 3.2e-30;					
Matches 238; Conservative	0; Mismatches 93; Indels 1; Gaps 1;					
157	tattcttcacgttgtaattcaactcgtttccaattcatgcgaaty-gtccatcata	215				
436	TCATTATTTACTTGCGAGCTGCACCTCATTAACATTTCTTGACACGCCACCACTCATTA	437				

QY	216	accgcacaaiaaiaatttttttggigtcttcaaaataaccacatttaacatca	275
Db	436	ATGCATTGTGTGCTCTCAATTTTTTCTGCTGTGATACAAAGCTTGATACCTTCATGATATTG	377
QY	276	laatctctatactcgigtgctcttgaatctctgaanaaaaagctgaaaagggcga	335
Db	376	CAGTTCCTATAGCCACGCTCCTCTTTTCCATCTCGAAACAAAGCTGAGAGGGGGCGAA	317
QY	336	gcaagacctcttccacatggggggccatctgctcttctgtcatctgaaggaac	395
Db	316	GAAGAAGCCTTCTCCCTGCAAGTGCACCTACTCTGTGTCTCTGTTCATGAACTC	257
QY	366	tgaatctcaatgatgtgctccatgcatcttgcttagctgaagacaaagaatgatt	455
Db	256	TCTTCTTATGACTGAGCCCTGGGTGTGAGCAAGTAATATMAAATATAGATGATT	197
QY	456	ctcgtgtttacagatataatccccgca	487
Db	196	CTCTGTTTACACCATTTGTGATTCCTCACTA	165

LOCUS	AG136576	681 bp	DNA	linear	GSS 04-NOV-2001				
DEFINITION	Pan troglodytes DNA, clone: PTB-150D04.R, genomic survey sequence.								
ACCESSION	AG136576								
VERSION	AG136576.1	GI:16666254							
KEYWORDS	GSS; GSS (genome survey sequence).								
SOURCE	Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male								

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE

AUTHORS
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 681)

AUTHORS

TITLE	Author	Journal	Year	Volume	Page	DOI
Totoki, Y., Watanabe, H. and Sakaki, Y.						
Direct Submission						

JOURNAL

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

COMMENT
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
clones are derived from the chimpanzee BAC library PTB. This BAC end

clone tracking errors.
PRIMERS

LIBRARY
Vector : PKS145

R.Site 2 : Sac1.
Location/Qualifiers

inos

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/organism="Pan troglodytes"  
/db_xref="taxon:9598"
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/sex="male"
/cell_type="lymphoblast"

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BASE COUNT	247 a	117 c	143 g	173 t	1 others
ORIGIN					

100

Query Match 33.98; Score 165.2; DB 12; Length 681

Best Lc

Matches 245; Conservative 0; Mismatches 133; Indels 0; Gaps 0.

Qy 1 tgaagcacaatgtaacccttgcttataccagatgagatgccacaactcagcgctca 60
 |||||
 Db 426 TGAAGCACAATGTAACCTTACTTATTCAGCATTAAGACCAATGAGCTGATCAG 367
 Qy 61 gtgcgaagatattcaatgtaattgttctcgcacctctcgttcagtgatgact 120
 |||||
 Db 366 GGTATTAATCTGTGATTTCTAGTGGCCCTTCTTCATGCTTAATTCATGCAAGGTTTTTT 307
 Qy 121 atgcgacaactctctgcaggtttatacatacatattctactgtgaatttaca 180
 |||||
 Db 306 AAGACATTAACCTTCTGTATTCACACACATACATCACTTTACTGTGACATTTATCC 247
 Qy 181 actgtcaaatattcaatgtaattgttctcgcacctctcgttcagtgatgact 240
 |||||
 Db 246 ATGTTAAATTTCTGTATTCATGATTTCTTACTACTTCCAAATGCTTTTATTTTCTC 187
 Qy 241 tgccttatacaaatccacatttaatacattacatacctcttatacctcgtgtct 300
 |||||
 Db 186 ATGTTAAATTTCAAGTTTCAACCATTTGGACCTGTTGTATTCATCAATTTCTCTCTC 127
 Qy 301 tgaattctgaaataaagcttgaataaaggcagaagcagcctctcagcagcgcg 360
 |||||
 Db 126 TACAATCTTGAATAAAGATCTGTCAAAAGACATTAAGAAAGCCTTCACACCTGTGGAGC 67
 Qy 361 ccaatcgtctctgtctc 378
 |||||
 Db 66 TCTCGAGCATGTAGCGC 49

RESULT 5
 LOCUS AZ090010 570 bp DNA linear GSS 08-MAY-2000
 DEFINITION RPCI-23-470116.TV RPCI-23 Mus musculus genomic clone RPCI-23-470116
 , DNA sequence.
 ACCESSION AZ090010
 VERSION AZ090010.1 GI:7732053
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 570)
 Zhao,S., Nierman,M., Feldblyum,T., Malek,J., Shatsman,S., Akintet
 , B., Levins,M., McGinn,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
 and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-470116.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@edj.med.bufileo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.bufileo.edu/orderingframe.htm)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
 http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html
 Plate: 470 row: I column: 16
 Seq primer: 17
 Class: BAC ends.

FEATURES
 Source location/Qualifiers

1..570
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-470116"
 /clone_lib="RPCI-23"
 /sex="female"
 /lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1:
 ECoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBAC3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 155 a 108 c 88 g 219 t
 ORIGIN

Query Match 33.0%; Score 160.8; DB 12; Length 570;
 Best Local Similarity 64.5%; Pred. No. 8.9e-28;
 Matches 240; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 116 ttactatgagcaactctctgcaggtttatacatacatattctactgtgaatt 175
 |||||
 Db 2 TTTCTATTACTCTAATACTTGTATTCATTAATGATGATCACTTTTCTGTGACATC 61
 Qy 176 ttacaactgtcaaatattcaatgtaattgttctcgcacctctcagcactaataatt 235
 |||||
 Db 62 GTTCCATTGCTGAAGATTTCCGTACTGACTACTTAAATTTCACTGATATTGTT 121
 Qy 236 ttgtgtctttatacaaatccacatttaargactataatctctatactcgtgtg 295
 |||||
 Db 122 TTAGCTGGAATTAATTCACCTCCTCACCGTTGTGATTTGTTCTGTACTACTTTTG 181
 Qy 296 cctttgatattctgaaataaagcttgaataaaggcagaagcagcctctcagcagcg 355
 |||||
 Db 182 CTATTGACGATTTTGAAGAAGATCTGTCCAAAGCATTAAGAAAGCCTTCTCTACTCT 241
 Qy 356 ggcgcacatctgtctctcgttcacattgtactacggaactctcgttcagtgatg 415
 |||||
 Db 242 GGAGCCATCTCTTAATCTGTCTGTCTGATGAGCCCTCTTCATGATATTGTTTC 301
 Qy 416 cctgcactcgtctgtcgtgaagacagcaagtgatctctcgttttaccagattata 475
 |||||
 Db 302 CCCGTGCCCAAGAGACAGATGTCAGATATCATAGACTCTGTCTTTACAGGTAATA 361
 Qy 476 attccctcgcta 487
 |||||
 Db 362 ATTCCGTGTGTTA 373

RESULT 6
 LOCUS AZ880560 404 bp DNA linear GSS 05-MAR-2001
 DEFINITION RPCI-23-18514.TJ RPCI-23 Mus musculus genomic clone RPCI-23-18514,
 DNA sequence.
 ACCESSION AZ880560
 VERSION AZ880560.1 GI:13199505
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 404)
 Zhao,S., Nierman,M., Feldblyum,T., Malek,J., Shatsman,S., Akintet
 , B., Levins,M., McGinn,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
 and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-18514.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cfo.org). Clones may be purchased from BACPAC

DB 147 AGTCTTCCCTGATATTAATGAAGTATCTTTATTTTATACGGTGTGATCCCATG 88
 OY 485 ct 486
 DB 87 TT 86

RESULT 8
 A0984439/c
 LOCUS A0984439 550 bp DNA linear GSS 30-JAN-2000
 DEFINITION RPCI-23-322E11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-322E11
 , DNA sequence.
 ACCESSION A0984439
 VERSION A0984439.1 GI:6817644
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 550)
 Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S., Aklnet
 and Fraser,C.M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
 and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSS: RPCI-23-322E11.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@med.bufileo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.bufileo.edu/orderingframe.htm)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
 http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 Plate: 322 row: E column: 11
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 1..550
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-322E11"
 /clone_11b="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1:
 EcorI, Site: 2: EcorI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcorI and EcorI Methylase. Site
 selected DNA was cloned into the pBAC3.6 vector at the
 EcorI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 189 a 110 c 115 g 136 t
 ORIGIN

Query Match 28.4%; Score 138.2; DB 12; Length 550;
 Best Local Similarity 56.5%; Pred. No. 1.8e-22;
 Matches 257; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

OY 32 gtgatgatgtccacaactcagcgtcagtcgaatattcattatgtgttc 91
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 548 GTCATTATGTCACAGAGGTGTGTCAGTTGTCATGACGACCTTATCTTACGCTGCT 489
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 92 ctgcatctctgtgttcagtgttacctatgtgcactacttctgcaggttaacata 151
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB 488 ATAAACATCCACATCATACAACTGACCTTTGCTTACCGTCTGCTGTTCAAAATACC 429
 OY 152 atcaattattctactgtgaatattacacgttccaattcaatgacatc 211
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 428 ATCAACGATTTTCTGTGATGTTTCCACATGCTTTTATGATGTCGTCACACATGG 369
 OY 212 altacgcactaataatatttlttgggtctttatatacaaacacttaagt 271
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 368 ATTACAAAGTAGTACTTTTGTCTGCGTGGAGTATAGTGTTCCAGTGGCTTGATA 309
 OY 272 atcaataatcttataactcgtgtgtcttcttgaatctggaaaaaagtctgaagaagc 331
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 308 ATCATAGTTCTCATGTGTGATCTGTGGCTGATCTTGAAGATCAACACTGCTGATGG 249
 OY 332 agaaagcaagccttcacacatgcgagccacatcgtcttcgtctcattgaactcga 391
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 248 ACACAGAAAGCCTTCTCCACGTTCTTCTACACGCGACGCTGTCAATTTTATGGC 189
 OY 392 actctgactctcaatgtagtgcgtcgtcatctggtcctgaagacaagaatg 451
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 188 ACTCTTTCTTCATATATGTTGGCCTTAATGCAAGTTCTTCCCTAGATTTATTAAGTG 129
 OY 452 tatctcgtttacagatataatccctgc 486
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 128 ATCTCTTATTTATACGGTGTGATCCCATGTT 94

RESULT 9
 A2714202/c
 LOCUS A2714202 556 bp DNA linear GSS 24-JAN-2001
 DEFINITION RPCI-24-86K20.TJ RPCI-24 Mus musculus genomic clone RPCI-24-86K20,
 DNA sequence.
 ACCESSION A2714202
 VERSION A2714202.1 GI:12449680
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 556)
 Zhao,S., Nierman,W., Malek,J., Shatsman,S., Aklnet,B., Levins,M.,
 Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregorjis,E.,
 Russell,D., de Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1999)
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@med.bufileo.edu). Clones may be purchased from BACPAC
 Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
 page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 Plate: 86 row: K column: 20
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 1..556
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-86K20"
 /clone_11b="RPCI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTARBAC1; Site: 1: BamHI; Site: 2: BamHI;
 RPCI-24 Mouse BAC library produced by Pieter de Jong. The
 library was cloned in the pTARBAC1 cloning vector at the
 BamHI sites using MhoI partially digested male C57BL/6J

BASE COUNT 184 a 103 c 136 g 133 t
ORIGIN

Query Match 26.7%; Score 129.8; DB 12; Length 556;
Best Local Similarity 54.5%; Pred. No. 1.7e-20;
Matches 260; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 11 tgaatcccttgccttataccagtgatgtccacaactcagctcagtgtaagt 70
DB 535 TGTAAACCCCTTGCTATCAATGCTATGATGCTCATCAAGCTGACACCTGATGATATT 476
QY 71 attcaatgaatgtgttccctgcacccctcgtgtcatgtgagttacatgtcgagcta 130
DB 475 GGGGTGATAGCATGGGTTTATTTGTTGCCACAGCTCACACAGTGTGCTAAGAGTC 416
QY 131 acctctgcaggtttaacataacatattctctactgtgaatttacaactgtcaaa 190
DB 415 CATTCTGTGAAGTGTGATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 356
QY 191 attcagcaatgtgcatctatataacgaactaataattattttgtgtcttata 250
DB 355 CTTTCTTGCTCCCTACTTTTATCAATGAGTGTGCTATGCTTATGCTTTCAT 296
QY 251 caataacccttaatgaatataatctctatctactgtgtgtcttattatctg 310
DB 295 ATCCTTTTCCCAACACGATGATGCTGCTTACATCTTCAATGCCAGCATCTTC 236
QY 311 aaaaaaaagtcgaaagggcagaagaagccttctccacatgctgagccatctgt 370
DB 235 CGTATTTAAATCCACTGAAGCAGGTCCAAAGCCTTTCAGACCTGCACCTCACATACAA 176
QY 371 tctgtctcatgtactcggaaactcgtatctcattcattgtgtgtcctgcactgctta 430
DB 175 ACTGATGCTGTGCTTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 116
QY 431 gctgaagcacaagaagaagtgatctctctgtttaacacagttataatccctgcta 487
DB 115 TCCATGACCAAGGAAAGTCTCTCTGATTTTATTCACATTTGTTGCCATGCTA 59

RESULT 10
BH342817/c 649 bp DNA linear GSS 03-DEC-2001
LOCUS
DEFINITION CH230-64F1, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH342817
VERSION BH342817
KEYWORDS
SOURCE GSS.
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 649)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
A., Gebregorjis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcorI segment
Unpublished (1999)
Other GSS: CH230-64F1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 64 Row: F Column: 1
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. 649
/organism="Rattus norvegicus"
/strain="BN/SSHsd/MCM"
/db_xref="taxon:10116"
/clone="CH230-64F1"
/clone_11b="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pFARBAC2.1. Site_1: EcorI. Site_2: EcorI;
CHORI-230 Rat (BN/SSHsd/MCM) BAC library produced by
Pieter de Jong"

BASE COUNT 219 a 124 c 150 g 156 t
ORIGIN

Query Match 26.5%; Score 129.2; DB 12; Length 649;
Best Local Similarity 55.6%; Pred. No. 2.4e-20;
Matches 270; Conservative 0; Mismatches 213; Indels 3; Gaps 1;

QY 1 tgaagcatatgatatccctgtcttataccagtgatgtccacaactcagcgctca 60
DB 550 TGTGCTCATGCTGAAGCCCTGCTTTCACAGTACCATGTCCTCATGAGGTGCTCCACTT 491
QY 61 gtgcataagttatcataatgaattgtttccctgcacccctcgtgttcatgtgattact 120
DB 490 GATCATTTGTGGGGGTATGTAATGGGGTTTGTGTGTCATGGCCATGGCCATGACGTAGT 431
QY 121 attgagactaacttctgcaggtttaacataacatattctactgtgaattaca 180
DB 430 TTTAACATGACCTTCTGTGATGCAACATCATCAATCAATCAATCAATCAATCAATCAAT 371
QY 181 acgttcaaaattcagaatgtgcatctcattataacgaactaataattatttttg 240
DB 370 TCTGAGAACTCTCTGCAACAGCACCCTCCAGCAATGAGCTGTGCTTTCATTTTGT 311
QY 241 tgccttatacaaatcaccacttaatgaactatcataatcctctatactcgtgtgctct 300
DB 310 GGGTGTCAATGTATATTAATCAATGACATGACATGCTTGTTCCTTACACCTTGATCCTTTC 251
QY 301 tgatatctcgaaaaaaagtcgaaagggcagaagaagccttctccacatgctgcgc 360
DB 250 CAACATCTCTGACATTCCTCTGCGAAGGTCCTCAAAAAGCCTTCAGAAACCTGTGCTC 191
QY 361 ccatctgcttctgtcctatgtactcaggaactcgtatctcattatgtatgtgctctgc 420
DB 190 CCATGTAGCAGCTGTCTTCTTCTTCTGAGCTGTGAGCTTCAATGATTTAAAGCTT 131
QY 421 atctgctatgtcgaagcacaagaagtgatctcgtgttatacagatlaatactc 480
DB 132 -TCTAAGCAACCTGTATGATGAAGAAATCTACATTTTATACATTTGTTGGGTTC 74
QY 481 cctgct 486
DB 73 AATGCT 68

RESULT 11
BH109232/c 763 bp DNA linear GSS 19-JUL-2001
LOCUS
DEFINITION RPI-24-352115, TVB RPI-24 Mus musculus genomic clone
ACCESSION BH109232
VERSION BH109232
KEYWORDS
SOURCE GSS.
ORGANISM house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 763)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.,
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-352115.TJB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@ligr.org

TITLE
JOURNAL
COMMENT

Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end
page: http://www.ligr.org/lbd/bac_ends/mouse/bac_end_intro.html
Plate: 352 row: 1 column: 15
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..763
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-352115"
/clone_11b="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pPRABAC1; site.1: BamHI; site.2: BamHI;
RPCI-24 Mouse BAC library produced by Pieter de Jong. The
library was cloned in the pPRABAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

BASE COUNT 265 a 108 c 133 g 257 t
ORIGIN

Query Match 26.0%; Score 126.8; DB 12; Length 763;
Best Local Similarity 58.2%; Pred. No. 8.8e-20;
Matches 241: Conservative 0; Mismatches 172; Indels 1; Gaps 1;

```

Oy 75 catatgaattgttcctccatcctcctcgttcacatgagttacatgacactt 134
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 75b CCTACATACAGGAGGACCTACATTCATGATTCACATGAGGTTCTTTCAGTTACTT 699
Oy 135 tctgaaggttaacataacataatcttctactgtgaatttacaactgttcaaat 194
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 698 TCTGACGCTCAGCAATCAAGCACTTCTTTGGATGTCCTCCCTCAACAGAACCTCT 639
Oy 195 catgcaatggtccatc-tattaagcactaataatatttctgtgtctttatacaa 253
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 638 CATGTGGTTGACCTTATATCAATGATGATGATCACTATTTTCTGGTTCACCTCAA 579
Oy 254 ataccacttaatactacatactactactcgttctgtcctcttgaattctgaa 313
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 578 ACTTTTACATTAATAGTCTCTCATTTCTTATATCTGATCTCTTTTACTATATTCACA 519
Oy 314 aaaaagctgaaaagggcagaagcaagcctctccacacatgcgagcccatctgtctt 373
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 518 ATGAGTCCAGAGGAGGAGCAAGGCTTATCTACTTGTGCAATCCACACTTTCGTCT 459
Oy 374 gttcattgactacggaactctgatactcatgatatgtgcgtccgcacatcgcttagct 433
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 438 GTGTAAATATTTCTGCTCTCTCTCATGATGATATTCGACAAAGTTCACTTAATGA 399
Oy 434 gaagacaagacaagatgtatctctgttttacaatataatccctcgta 487
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 GGGTATTAAGACATACCTGTCTATATTTTACTCTAGTAATTCCTTTATTA 345

```

RESULT 12

AZ103967/c 611 bp DNA linear GSS 09-MAY-2000
LOCUS
DEFINITION
RPCI-23-33618.TV RPCI-23 Mus musculus genomic clone RPCI-23-33618,
DNA sequence.

ACCESSION
AZ103967
VERSION
AZ103967.1 GI:7757025
KEYWORDS
GSS.
SOURCE
house mouse.
ORGANISM
Mus musculus

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 611)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret,
B., Levins, M., McGinn, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.,
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-33618.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@ligr.org

TITLE
JOURNAL
COMMENT

Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.html>)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.ligr.org/lbd/bac_ends/mouse/bac_end_intro.html
Plate: 33 row: 6 column: 18
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..611
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-33618"
/clone_11b="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site.1:
EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 206 a 113 c 142 g 150 t
ORIGIN

Query Match 25.9%; Score 126; DB 12; Length 611;
Best Local Similarity 53.7%; Pred. No. 1.4e-19;
Matches 261: Conservative 0; Mismatches 225; Indels 0; Gaps 0;

```

Oy 1 ttagcatatgtaatcccttgcttaccagtgatgattccaaacacagcgctca 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 571 TGCACCATATGTAAGCCCTTGCTGTACACATTATATGTCCTCCACATCTCTGTCTT 512
Oy 61 gttgtaagtattcatatgtaattggtttctcgtacactcgtgttcattgagttaact 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 511 ATTGTTATTTGGGCTTATATGCCATTGCTCTTATAGTAAGTAACACACACACACTTTGAC 452
Oy 121 attgcgaatactcttcaggtttaacataataatattctactgtgaatttaca 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 451 CTTTGTCTTACATCTCTGTGTCATATATATCAACACACTTTTCTGTGACATTTGCC 392
Oy 181 actgtcaaaatttcagcaatggtccatctattaaagcactaataatatttctgg 240

```



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Db      391  ATTGCTGCTCTGACATGTTCTGACACCCACATAAATAAGTGGTCTTTTGTCTGGC 332
Qy      241  tgcattatacaatacccccttaagactatcatactctctactcgtgtgcctt 300
Db      331  TGGCAGAGTGGTGTCTGACGTGACATATTCCTGCTCATATGTTGCACTTGAA 272
Qy      301  tgatatctgaaaaaagctgaagaaggcagaagaagccttcacatgcgagc 360
Db      271  GGCATTTTGAAGATTGACAGCAGCAATGGGAGACGAAAGCCTTTCACACTTCTC 212
Qy      361  ccactcgtcttcgtcctcattgactacggaactcgtatctcattgctgcctgc 420
Db      211  TCACTTGGCAACTGCTCTCTATCCGTATGGAGCTTTTCTTCATCTATGTTAGACCCA 152
Qy      421  atctgcttgcgtgaagaccagaagaagtgatctcctcgttttaacgattatcc 480
Db      151  TGTCACTTCTCTGTAATTAATAAGATCTTTATTTTACACGATGGTGAATTC 92
Qy      481  cctgct 486
Db      91  CATGTT 86

RESULT 13
A2560017/c 507 bp DNA linear GSS 20-NOV-2000
LOCUS      RPCI-23-216D21.TV RPCI-23 Mus musculus genomic clone RPCI-23-216D21
DEFINITION
            ' DNA sequence.
ACCESSION  A2560017
VERSION     A2560017.1 GI:11239837
KEYWORDS   house mouse.
SOURCE      Mus musculus.
ORGANISM   Mus musculus.
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            Zhao, S., Niernan, W., Feldblum, T., Malek, J., Shatsman, S., Aklnret
            B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
            and Fraser, C.M.
            Mouse BAC End Sequences from Library RPCI-23
            Unpublished (1999)
            Other GSSs: RPCI-23-216D21.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieterdejong.med.bufileo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.bufileo.edu/orderingframe.htm)
            or from Resea.ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html
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            Seq primer: T7
            Class: BAC ends.

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                /sex="Female"
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                /note="Organ: Kidney/Brain: Vector: pBACE3.6; Site_1:
                EcORI; Site_2: EcORI; Female C57BL/6J mouse kidney and/or
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                selected DNA was cloned into the pBACE3.6 vector at the

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            EcoRI sites. The ligation products were transformed into
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Query Match      25.5%; Score 124.4; DB 12; Length 507;
Best Local Similarity 53.5%; Pred. No. 3.2e-19;
Matches 260; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

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Qy      61  gtgtcagaatattcattgaattgatttccgcacccctcgttcaigtgattact 120
Db      428  ATTGTTGGGAATATCCATATGTTGGTGGTGTGTAATGTTGGACATTTACTGTTGTGT 369
Qy      121  atgcgaactaacttcgcaggtttaacataatattctactcgtgaattaca 180
Db      368  GTTAAGTCTGTGCTTCTGTGTGACCACTCAGATTAATCATTCTTCTGTGACTTCTCCC 309
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Db      308  TTTGCTGAAGAGTGTCTGTGACATGTCCTCATATTGGAATCATCCCGTATCTCTTC 249
Qy      241  tgcattatacaataaccacttaagactatcatactctactcgtgtgcctt 300
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Qy      301  tgatatctgaaaaaagctcgaagaaggcagaagaagccttcacatgcgagc 360
Db      188  CACCATCTCTGAAGATGGGCTCTCACTGAGGGCCGACACAAAGCCTTCTCCACTGCACTC 129
Qy      361  ccactcgtcttcgtcctcattgactacggaactcgtatctcattgctgcctgc 420
Db      128  CCACCTCAGTGCAGTCACTGCTCTTATGGGACCATTAACGCTTAACGAGCCCAA 69
Qy      421  atctgcttgcgtgaagaccagaagaagtgatctcctcgttttaacgattatcc 480
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Qy      481  cctgct 486
Db      8  TATGTT 3

RESULT 14
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LOCUS      RPCI-23-26C8.TV RPCI-23 Mus musculus genomic clone RPCI-23-26C8,
DEFINITION
            DNA sequence.
ACCESSION  A2086388
VERSION     A2086388.1 GI:7728122
KEYWORDS   house mouse.
SOURCE      Mus musculus.
ORGANISM   Mus musculus.
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            Zhao, S., Niernan, W., Feldblum, T., Malek, J., Shatsman, S., Aklnret
            B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
            and Fraser, C.M.
            Mouse BAC End Sequences from Library RPCI-23
            Unpublished (1999)
            Other GSSs: RPCI-23-26C8.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 27, 2002, 11:17:12 ; Search time 1801.95 Seconds
(without alignments)
5635.664 Million cell updates/sec

Title: US-09-747-155-224

Perfect score: 487
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	487	100.0	487	6	AX181436	AX181436 Sequence
2	487	100.0	487	6	AF179759	AF179759 Homo sapi
3	486	99.8	486	6	AX242110	AX242110 Sequence
4	236	48.5	485	6	AX181383	AX181383 Sequence
5	236	48.5	485	6	AF179729	AF179729 Pan trogl
6	185	38.0	487	6	AX181394	AX181394 Sequence
7	185	38.0	487	6	AF179735	AF179735 Pan trogl
8	30	6.2	927	10	AY073094	AY073094 Mus muscu
9	30	6.2	138556	2	AC105564	AC105564 Rattus no
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13	26	5.3	930	10	AY073315	AY073315 Mus muscu
14	23	4.7	71291	9	AC090115	AC090115 Homo sapi
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37	20	4.1	150442	2	AC022782	AC022782 Mus muscu
38	20	4.1	159453	2	AC006732	AC006732 Caenorhab
39	20	4.1	167596	30	AC016137	AC016137 Homo sapi
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42	20	4.1	169234	3	CNS06C70	AL390799 Human chr
43	20	4.1	170288	3	AC023694	AC023694 Drosophila
44	20	4.1	192178	2	AC009443	AC009443 Homo sapi
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ALIGNMENTS

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LOCUS AX181436 487 bp DNA linear PAT 07-AUG-2001
DEFINITION Sequence 224 from Patent WO0146262.
ACCESSION AX181436
VERSION AX181436.1 GI:15141548
KEYWORDS
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ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 487)
Rouquier, S. and Giorgi, D.
Olfactory receptor genes and pseudogenes in primates and mouse
Patent: WO 0146262-A 224 28-JUN-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 ccactgctcttcgtctcattgtaactgaagactgactcttaagtatgctgctgc 420

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OY 481 cctgcta 487
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DB 481 cctgcta 487

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LOCUS Homo sapiens olfactory receptor (HSA1) gene, partial cds.
DEFINITION AF179759
ACCESSION AF179759
VERSION AF179759.1 GI:7211526
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Rouquier, S., Blancher, A. and Giorgi, D.
TITLE The olfactory receptor gene repertoire in primates and mouse:
evidence for reduction of the functional fraction in primates
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2870-2874 (2000)
MEDLINE 20183981
REFERENCE 2 (bases 1 to 487)
AUTHORS Giorgi, D.G. and Rouquier, S.P.
TITLE Direct Submission
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JOURNAL Submitted (24-AUG-1999) Institut de Genetique Humaine, CNRS, UPR
1142, rue de la Cardonille, Montpellier Cedex 5 34396, France
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DB 61 gttgcgaagatttcatatgattgattgcttccgcattccttgctcagtgagttact 120

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DB 481 cctgcta 487

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DEFINITION Sequence 858 from Patent WO0127158.
ACCESSION AX242110
VERSION AX242110.1 GI:15798985
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
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REFERENCE 1 (bases 1 to 486)
AUTHORS Bellenson,J., Smith,D., Lancel,D., Glusman,G., Fuchs,T. and Yanai,I.
TITLE Olfactory receptor sequences
JOURNAL Patent: WO 0127158-A 858 19-APR-2001;
Discents (US) ; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
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Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TTGCTAAGATATTCATATGTAATGTTTCTGCTGATCCTCTGATGATGATTTACTA 120

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QY 482 ctgcta 487
DB 481 CTGCTA 486

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LOCUS AX181383
DEFINITION Sequence 171 from Patent WO0146262.
ACCESSION AX181383
VERSION AX181383.1 GI:15132985
KEYWORDS
SOURCE chimpanzee.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
REFERENCE 1 (bases 1 to 485)
AUTHORS Rouquier,S. and Giorgi,D.
TITLE Olfactory receptor genes and pseudogenes in primates and mouse
JOURNAL Patent: WO 0146262-A 171 28-JUN-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
location/Qualifiers

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Matches 436; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 121 atcgcaactcttcagaggtttaacataataattctcagtggaatttaaa 180
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QY 181 actgtcaaatattcatgcaatggtccatctatlaacgacataataattatttgg 240
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QY 361 ccactgcttctgctcactgtaactgtaactgctcactgtaactgtaactgta 420
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ACCESSION AF179729
VERSION AF179729.1 GI:7211473
KEYWORDS
SOURCE chimpanzee.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
REFERENCE 1 (bases 1 to 485)
AUTHORS Rouquier,S., Blancher,A. and Giorgi,D.
TITLE The olfactory receptor gene repertoire in primates and mouse: evidence for reduction of the functional fraction in primates
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2870-2874 (2000)
MEDLINE 20183981
REFERENCE 2 (bases 1 to 485)
AUTHORS Giorgi,D.G. and Rouquier,S.P.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1999) Institut de Genetique Humaine, CNRS, UPR 1142, rue de la Cardonille, Montpellier Cedex 5 34396, France
location/Qualifiers

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gene
BASE COUNT 130 a 107 c 77 g 171 t
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DB 181 acgttcaaatcttcatatgcaatgctcattatgaacgaactaataatttttgg 240
OY 241 tgccttatacaaatcccaactttaagactatacatctctatactcgttgctctt 300
DB 241 tgccttatacaaatcccaactttaagactatacatctctatactcgttgctctt 300
OY 301 tgaattctgaaaaaaagtcgaaaggcagaagcaaaagccttccacatgcggcg 360
DB 301 tgaattctgaaaaaaagtcgaaaggcagaagcaaaagccttccacatgcggcg 360
OY 361 ccatcgcttctgcttcattgactacgaactcgaactcattatgtagtgcctcg 420
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OY 421 atcgtgcttagctgaagacc 440
DB 421 atcgtgcttagctgaagacc 440

RESULT 6
AX181394 487 bp DNA linear PAT 07-AUG-2001
LOCUS AX181394
DEFINITION Sequence 182 from Patent WO0146262.
ACCESSION AX181394
VERSION AX181394.1 GI:15141512
KEYWORDS
SOURCE
ORGANISM Chimpazee.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE
AUTHORS Rouquier,S. and Giorgi,D.
TITLE Olfactory receptor genes and pseudogenes in primates and mouse
JOURNAL Patent: WO 0146262-A 182 28-JUN-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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BASE COUNT 129 a 107 c 78 g 173 t
ORIGIN

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Best Local Similarity 98.9%; Pred. No. 2.1e-88;
Matches 435; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 61 gtgcgaatattcatatgtaattggttcctgcacatcccttggttcattgagttact 120
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DB 121 atgcgaactaacttctgcaggtttaacataacatacttactgtaatttaca 180
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DB 301 tgaattctgaaaaaaagtcgaaaggcagaagcaaaagccttccacatgcggcg 360
OY 361 ccatcgcttctgcttcattgactacgaactcgaactcattatgtagtgcctcg 420
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OY 421 atcgtgcttagctgaagacc 440
DB 421 atcgtgcttagctgaagacc 440

RESULT 7
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LOCUS AF179735
DEFINITION Pan troglodytes olfactory receptor (PTR210) gene, partial cds.
ACCESSION AF179735
VERSION AF179735.1 GI:7211484
KEYWORDS
SOURCE
ORGANISM Chimpazee.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE
AUTHORS Rouquier,S., Blancher,A. and Giorgi,D.
TITLE The olfactory receptor gene repertoire in primates and mouse:
evidence for reduction of the functional fraction in primates
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2870-2874 (2000)
MEDLINE 20183981
REFERENCE
AUTHORS Giorgi,D.G. and Rouquier,S.P.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1999) Institut de Genetique Humaine, CNRS, UPR
1142, rue de la Cardonille, Montpellier Cedex 5 34396, France
FEATURES
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Rutz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shooshitari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swatek, A., Taber, P., Tamerisa, A., Thomas, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wellington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 138556)
Worley, K.C.
Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

----- Genome Center of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GNEZ
Center clone name: CH230-250G11

----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to findPhrapList

Consensus quality: 104982 bases at least Q40
Consensus quality: 113437 bases at least Q30
Consensus quality: 120052 bases at least Q20
Estimated insert size: 98776; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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63900 66087: contig of 4088 bp in length
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Alsbrooks, S. L., Amaralunge, H. C., Are, J. R., Banks, T., Barbara, J., Benton, J., Blmage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N. P., Buhay, C.,

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* 107022 107122: gap of unknown length
* 107122 116733: contig of 9612 bp in length
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Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 152 ataccattattctactgtgaattttaca 180
Db 57737 ATACATTATTCTACTGTGAATTTTACA 57765

RESULT 12
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LOCUS Mus musculus olfactory receptor MOR182-8 pseudogene, partial
DEFINITION
ACCESSION AY074074
VERSION AY074074.1 GI:18481236
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 919)
AUTHORS Zhang, X. and Firestein, S.
TITLE The olfactory receptor gene superfamily of the mouse
JOURNAL Nat. Neurosci. 5 (2), 124-133 (2002)
PUBMED 11802173
ADAMS, M.
REFERENCE 2 (bases 1 to 919)
AUTHORS Adams, M.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2002) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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DEFINITION
ACCESSION AY073315
VERSION AY073315.1 GI:18479927
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 930)
AUTHORS Zhang, X. and Firestein, S.
TITLE The olfactory receptor gene superfamily of the mouse
JOURNAL Nat. Neurosci. 5 (2), 124-133 (2002)
PUBMED 11802173
ADAMS, M.
REFERENCE 2 (bases 1 to 930)
AUTHORS Adams, M.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2002) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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LOCUS Homo sapiens 12q RP11-762h13 (Roosevelt Park Cancer Institute
DEFINITION Human BAC Library) complete sequence.
ACCESSION AC090115
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VERSION AC090115.15 GI:15808446
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C., Alshrook,S.L., Amaralung,H.C., Are,J.R., Banks,T., Barbata,J., Bantson,J., Bimaga,K., Blankenburg,K., Bonin,D., Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathore,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Demn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guenara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huylk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichteage,O., Lien,C., Liu,J., Liu,W., Louisedge,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Maronde,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nockenko,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Perez,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L., Qullis,M., Ren,Y., Rives,M., Rojas,A., Rojokhan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shooshitari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Ver,V., Villalón,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorilla,S., Zscherpelat,R., Weinstein,G. and Gibbs,R.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 71291)
 AUTHORS Morley,K.C.
 JOURNAL Direct Submission
 REFERENCE Submitted (17-FEB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 TITLE 3 (bases 1 to 71291)
 AUTHORS Morley,K.C.
 JOURNAL Direct Submission
 REFERENCE Submitted (29-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 COMMENT On Sep 29, 2001 this sequence version replaced gi:15559142.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the features listing.

ANNOTATION OF FEATURES:
 STRS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
 Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
 Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
 SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
 QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.
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repeat_region /rpt_family="L1PA13"
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repeat_region /rpt_family="L1ME1"
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repeat_region 26818, .27134
repeat_region /rpt_family="AlusX"
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repeat_region /rpt_family="MSTA"
repeat_region complement(27779, .28324)
repeat_region /rpt_family="MER67D"
repeat_region complement(29282, .29364)
repeat_region /rpt_family="MIR"
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repeat_region complement(32157, .33408)
repeat_region /rpt_family="L2"
repeat_region 33570, .33875
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repeat_region 36055, .36084
repeat_region /rpt_family="AT_rich"

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Query Match 4.7% Score 23; DB 9; Length 71291;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 329 ggcagaagcaagccttcac 351
DB 6390 GCCAGAGCAAGCCTTCAC 6412

```

```

RESULT 15
AC105564 138556 bp DNA linear HTG 09-JAN-2002
LOCUS Rattus norvegicus clone CH230-250G11, *** SEQUENCING IN PROGRESS
DEFINITION *** 60 unordered pieces.
AC105564
VERSION AC105564.1 GI:18092786
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

REFERENCE

1 (bases 1 to 138556)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsprouks,S.L., Amarantunge,H.C., Are,J.R., Banks,T., Barbarta,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowe,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Den,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferriguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Hollway,C., Hollins,B., Homsf., Howard,S., Huber,J., Hui,Y.S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,D., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louisedge,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,D., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nickerson,E., Nwokwenwo,S., Oguh,M., Okunou,G., Orangunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojurokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,R., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,K., Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 138556)

Worley,K.C.

Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

----- Genome Center of Medicine

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GNEZ

Center clone name: CH230-250G11

----- Summary Statistics

Assembly program: Phrap; version 0.990329first call to findPhraplist

Consensus quality: 104982 bases at least Q40

Consensus quality: 113437 bases at least Q20

Consensus quality: 120052 bases at least Q20

Estimated insert size: 98776; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 1.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drafc_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 60 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1	12026:	contig of 12026 bp in length
*	12027	12126: gap of unknown length
*	12127	17583: contig of 5457 bp in length
*	17584	17683: gap of unknown length
*	17684	22927: contig of 5244 bp in length
*	22928	23027: gap of unknown length
*	23028	27987: contig of 4960 bp in length
*	27988	28087: gap of unknown length
*	28088	32504: contig of 4417 bp in length
*	32505	32604: gap of unknown length
*	32605	35333: contig of 2729 bp in length
*	35334	35433: gap of unknown length
*	35434	37327: contig of 1894 bp in length
*	37328	37427: gap of unknown length
*	37428	40912: contig of 3485 bp in length
*	40913	41012: gap of unknown length
*	41013	44129: contig of 3117 bp in length
*	44130	44229: gap of unknown length
*	44230	46597: contig of 2368 bp in length
*	46598	46697: gap of unknown length
*	46698	50418: contig of 3721 bp in length
*	50419	50518: gap of unknown length
*	50519	52990: contig of 2472 bp in length
*	52991	53090: gap of unknown length
*	53091	56522: contig of 3432 bp in length
*	56523	56622: gap of unknown length
*	56623	59005: contig of 2383 bp in length
*	59006	59105: gap of unknown length
*	59106	61667: contig of 2562 bp in length
*	61668	61767: gap of unknown length
*	61768	63889: contig of 2132 bp in length
*	63900	63999: gap of unknown length
*	64000	68087: contig of 4088 bp in length
*	68088	68187: gap of unknown length
*	68188	70694: contig of 2507 bp in length
*	70695	70794: gap of unknown length
*	70795	73386: contig of 2592 bp in length
*	73387	73486: gap of unknown length
*	73487	75692: contig of 2206 bp in length
*	75693	75792: gap of unknown length
*	75793	77929: contig of 2137 bp in length
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*	78030	79286: contig of 1267 bp in length
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*	82337	82238: contig of 2842 bp in length
*	82339	82338: gap of unknown length
*	84658	84658: contig of 2320 bp in length
*	84659	84758: gap of unknown length
*	84759	87336: contig of 2578 bp in length
*	87337	87436: gap of unknown length
*	87437	89496: contig of 2060 bp in length
*	89497	89596: gap of unknown length
*	89597	90917: contig of 1321 bp in length
*	90918	91017: gap of unknown length
*	91018	92625: contig of 1608 bp in length
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*	92726	93955: contig of 1230 bp in length
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*	95239	95338: gap of unknown length
*	95339	96506: contig of 1168 bp in length
*	96507	96606: gap of unknown length
*	96607	98414: contig of 1808 bp in length
*	98415	98514: gap of unknown length
*	98515	100270: contig of 1756 bp in length
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*	100371	101914: contig of 1544 bp in length
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*	104661	104760: gap of unknown length
*	104761	106384: contig of 1624 bp in length
*	106385	106484: gap of unknown length
*	106485	107638: contig of 1154 bp in length
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*	107739	109065: contig of 1327 bp in length
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*	109166	110732: contig of 1567 bp in length
*	110733	110832: gap of unknown length
*	110833	112101: contig of 1269 bp in length
*	112102	112201: gap of unknown length
*	112202	113509: contig of 1308 bp in length
*	113510	113609: gap of unknown length
*	113610	115100: contig of 1491 bp in length
*	115101	115200: gap of unknown length
*	115201	116535: contig of 1335 bp in length
*	116536	116635: gap of unknown length
*	116636	118099: contig of 1464 bp in length
*	118100	118199: gap of unknown length
*	118200	119225: contig of 1026 bp in length
*	119226	119325: gap of unknown length
*	119326	121099: contig of 1774 bp in length
*	121100	121199: gap of unknown length
*	121200	122556: contig of 1357 bp in length
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*	122657	124309: contig of 1653 bp in length
*	124310	124409: gap of unknown length
*	124410	125647: contig of 1238 bp in length
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*	125748	126786: contig of 1039 bp in length
*	126787	126886: gap of unknown length
*	126887	128160: contig of 1274 bp in length
*	128161	128260: gap of unknown length
*	128261	129777: contig of 1517 bp in length
*	129778	129877: gap of unknown length
*	129878	130976: contig of 1099 bp in length
*	130977	131076: gap of unknown length
*	131077	132445: contig of 1369 bp in length
*	132446	132545: gap of unknown length
*	132546	133844: contig of 1299 bp in length
*	133845	133944: gap of unknown length
*	133945	135012: contig of 1068 bp in length

Query Match 4.7%; Score 23; DB 2; Length 138556;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 326 aaggcagagcaagcctctc 348
|||||
Db 39119 AAGGCGAAGCAAGCCTTCTC 39097

Search completed: June 27, 2002, 13:08:47
Job time: 6695 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 27, 2002, 12:06:47 ; Search time 204.48 seconds

(without alignments)
4089.091 Million cell updates/sec

Title: US-09-747-155-224

Perfect score: 487

Sequence: 1 tgtagccataatgtaacccct.....cgattataatccctgcta 487

Scoring table:

OLIGO-MUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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N_Geneseq_032802.*
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4: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT:*
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23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	100.0	487	22	AAH84016
2	486	99.8	486	22	AAH32285
3	236	48.5	485	22	AAH83986
4	185	38.0	487	22	AAH83992
5	29	6.0	988	22	AAH32168
6	22	4.5	953	22	AA199556
7	19	3.9	915	22	AAH32012
8	19	3.9	915	22	AAH32436
9	19	3.9	918	22	AAH42358

10	19	3.9	1037	11	AA004705
11	19	3.9	1160	11	AA004706
12	19	3.9	1166	11	AA004704
13	19	3.9	4809	23	ABL14992
14	18	3.7	494	20	AA224554
15	18	3.7	494	21	AA065793
16	18	3.7	714	22	AA535473
17	18	3.7	778	22	AA536434
18	18	3.7	921	22	AAH31745
19	18	3.7	924	22	AA542225
20	18	3.7	924	22	AA542336
21	18	3.7	967	22	AAH31747
22	18	3.7	980	22	AA013713
23	18	3.7	980	22	AA013714
24	18	3.7	2411	23	ABL19014
25	18	3.7	2635	18	AA183966
26	18	3.7	5190	23	ABL05582
27	18	3.7	5277	23	ABL05572
28	18	3.7	5864	24	ABL33441
29	18	3.7	6060	18	AAV74845
30	18	3.7	8861	22	AA527785
31	18	3.7	580073	18	AA158840
32	17	3.5	119	21	AA024832
33	17	3.5	300	21	AA00216
34	17	3.5	315	22	AAK73673
35	17	3.5	317	22	AAK73674
36	17	3.5	317	22	AAK58786
37	17	3.5	400	18	AAV78417
38	17	3.5	420	20	AAH85057
39	17	3.5	476	22	AA543417
40	17	3.5	482	22	ABAT5636
41	17	3.5	482	22	ABA40244
42	17	3.5	482	22	AAK24238
43	17	3.5	482	22	AAK50274
44	17	3.5	482	22	AA127348
45	17	3.5	482	22	AA156232

ALIGNMENTS

RESULT 1	
AAH84016	AAH84016 standard; DNA; 487 BP.
AC	AAH84016;
XX	25-SEP-2001 (first entry)
DT	Human olfactory receptor encoding gene 4.
XX	
DE	Human olfactory receptor; primate; mouse; human; food processing industry;
XX	
KW	aromas; perfume; toxic substance; ds.
KW	
XX	
OS	Homo sapiens.
XX	
PN	WO200146262-A2.
PD	28-JUN-2001.
XX	
PF	22-DEC-2000; 2000WO-1B02017.
XX	
PR	22-DEC-1999; 99US-0171746.
PR	21-DEC-2000; 2000US-0747155.
PA	(CNRS) CNRS CENT NAT RECH SCI.
XX	
PI	Rouquier S, Giorgi D;
XX	
DR	WPI: 2001-381911/40.
DR	P-PSDB; AAG98521.
XX	
PT	Nucleic acids encoding primate and murine olfactory receptors, useful

PT for analysis odours e.g. in food processing and perfumery -
 XX
 XX
 PS Claim 1: Page 273-274; 482pp; English.

CC The invention relates to olfactory receptors (AMG98432-AMG98609) and the
 CC genes encoding them (AAH32285-AAH32286) including pseudogenes of 10
 CC prime species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours).

XX
 XX Sequence 487 BP; 131 A; 105 C; 77 G; 174 T; 0 other:

Query Match 100.0%; Score 487; DB 22; Length 487;
 Best Local Similarity 100.0%; Pred. No. 8.2e-234;
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tgaagcacaatgtaacccctgcttatacagatgatgltccacaacactcagcgctca 60
 |||||||
 DB 1 tgaagcacaatgtaacccctgcttatacagatgatgltccacaacactcagcgctca 60
 OY 61 gtgcgaagatctcatatgtaattgttccgcacccctcgtggtcattgaggttact 120
 |||||||
 DB 61 gtgcgaagatctcatatgtaattgttccgcacccctcgtggtcattgaggttact 120
 OY 121 attgcacactactctgcaggttaacataacattattctactgtaaaatttaca 180
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 DB 121 attgcacactactctgcaggttaacataacattattctactgtaaaatttaca 180
 OY 181 actgttcaaaattcattgcaatggtccatcatatcaacgacataatatttttgg 240
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 DB 181 actgttcaaaattcattgcaatggtccatcatatcaacgacataatatttttgg 240
 OY 241 tggctttatacaaatccacttaagtactatcataatctcttataactcgtgctctt 300
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 DB 241 tggctttatacaaatccacttaagtactatcataatctcttataactcgtgctctt 300
 OY 301 tgaattctgaaaaaaagctgaaaaaggcagaagaagcctctccacatgcgcgcc 360
 |||||||
 DB 301 tgaattctgaaaaaaagctgaaaaaggcagaagaagcctctccacatgcgcgcc 360
 OY 361 caactcgtcttctgctcattgtaactcgaactctgattctcattgtaattgctctgc 420
 |||||||
 DB 361 caactcgtcttctgctcattgtaactcgaactctgattctcattgtaattgctctgc 420
 OY 421 atttgcttaagctggaagcagaagaagtgtattctctgttttacaagataatttc 480
 |||||||
 DB 421 atttgcttaagctggaagcagaagaagtgtattctctgttttacaagataatttc 480
 OY 481 cctgccta 487
 |||||||
 DB 481 cctgccta 487

RESULT 2
 AAH32285
 ID AAH32285 standard; DNA; 486 BP.

XX AAH32285;

XX 30-JUL-2001 (first entry)

DE Human olfactory receptor polynucleotide, SEQ ID NO: 858.

XX Human, olfactory receptor; OR; primary scent determination;

KW secondary scent determination; polypeptide library; odour receptor;

XX scent profile; scent fingerprint; scent representation; ds.

OS Homo sapiens.

XX WO200127158-A2.

XX 19-APR-2001.
 PD
 XX
 XX 06-OCT-2000; 2000WO-US27582.
 PF
 XX
 PR 08-OCT-1999; 99US-0158615.
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 DR WPI; 2001-290713/30.
 XX
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 PS
 XX Claim 8: Page 523; 1857pp; English.

CC The present sequence is one of a number of isolated polynucleotides
 CC which encode polypeptides involved in olfactory sensation. The
 CC polynucleotides can be used in screening for olfactory agonists and
 CC antagonists. The methods allow for the determination of primary
 CC scents and the identification of the odour receptors used to detect
 CC these primary scents. The methods also enable determination of
 CC secondary scents and the identification of combinations of odour
 CC receptors that are involved in detecting such secondary scents.
 CC This enables the construction of a scent representation (also called
 CC a scent fingerprint or scent profile), which may be used to re-create
 CC and edit scents. Libraries of olfactory receptors are useful for
 CC determining the interaction pattern of a composition with the receptors,
 CC and can be used for determining differences in the olfactory faculties
 CC of different individuals.

XX
 XX Sequence 486 BP; 131 A; 105 C; 77 G; 173 T; 0 other:

Query Match 99.8%; Score 486; DB 22; Length 486;
 Best Local Similarity 100.0%; Pred. No. 2.6e-233;
 Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaagcacaatgtaacccctgcttatacagatgatgltccacaacactcagcgctca 61
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 DB 1 gtaagcacaatgtaacccctgcttatacagatgatgltccacaacactcagcgctca 60
 OY 62 ttgctaagatctcatatgtaattgttccgcacccctcgtggtcattgaggttact 121
 |||||||
 DB 61 ttgctaagatctcatatgtaattgttccgcacccctcgtggtcattgaggttact 120
 OY 122 ttgcaactaactctgcaggttcaacataacattattctactgtaaaatttaca 181
 |||||||
 DB 121 ttgcaactaactctgcaggttcaacataacattattctactgtaaaatttaca 180
 OY 182 ctggtcaaaattcattgcaatggtccatcatatcaacgacataatatttttgg 241
 |||||||
 DB 181 ctggtcaaaattcattgcaatggtccatcatatcaacgacataatatttttgg 240
 OY 242 gctttatacaaatccacttaagtactatcataatctcttataactcgtgctctt 301
 |||||||
 DB 241 gctttatacaaatccacttaagtactatcataatctcttataactcgtgctctt 300
 OY 302 gatattctgaaaaaaagctgaaaaaggcagaagaagcctctccacatgcgcgcc 361
 |||||||
 DB 301 gatattctgaaaaaaagctgaaaaaggcagaagaagcctctccacatgcgcgcc 360
 OY 362 catcgtcttctgctcattgtaactcgaactctgattctcattgtaattgctctgc 421
 |||||||
 DB 361 catcgtcttctgctcattgtaactcgaactctgattctcattgtaattgctctgc 420
 OY 422 tctggttaagctggaagcagaagaagtgtattctctgttttacaagataatttc 481
 |||||||
 DB 421 tctggttaagctggaagcagaagaagtgtattctctgttttacaagataatttc 480

OY 482 ctgcta 487
|||||
DB 481 ctgcta 486

RESULT 3

AAH83986
ID AAH83986 standard; DNA: 485 BP.

AC AAH83986;

DT 25-SEP-2001 (first entry)

DE Pan troglodytes olfactory receptor encoding gene 10.

XX Olfactory receptor; primate; mouse; human; food processing industry;

KW aromas; perfumery; toxic substance; ds.

XX Pan troglodytes.

PN WO200146262-A2.

PD 28-JUN-2001.

PF 22-DEC-2000; 2000WO-IB02017.

PR 22-DEC-1999; 99US-0171746.

PR 21-DEC-2000; 2000US-0747155.

XX (CNRS) CNRS CENT NAT RECH SCI.

PI Rouquier S, Giorgi D;

XX WPI; 2001-381911/40.

DR P-PSDB; AAG98501.

XX Nucleic acids encoding primate and murine olfactory receptors, useful

PT for analysis odours e.g. in food processing and perfumery -

PS Claim 1; Page 227; 482pp; English.

XX The invention relates to olfactory receptors (AAG98432-AA98609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours).

XX Sequence 485 BP; 130 A; 107 C; 77 G; 171 T; 0 other;

Query Match 48.5%; Score 236; DB 22; Length 485;

Best Local Similarity 99.1%; Pred. No. 3.5e-108;

Matches 436; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 tgaagcacaatgtaacccctgtcttaccagtgatgagtgacaaacaactcagcgctca 60

DB 1 tgaagcacaatgtaacccctgtcttaccagtgatgagtgacaaacaactcagcgctca 60

OY 61 gtgctgaagtattcatatgtaattggttccctgcacccctcgtgtcattgagatttact 120

DB 61 gtgctgaagtattcatatgtaattggttccctgcacccctcgtgtcattgagatttact 120

OY 121 attcgcaacttctcaggttaacataatacatattctcactgtgaatttaca 180

DB 121 attcgcaacttctcaggttaacataatacatattctcactgtgaatttaca 180

OY 181 actgttcaaaattcgaatgacatgacatatttaacgcaactaataattattttgg 240

DB 181 actgttcaaaattcgaatgacatgacatatttaacgcaactaataattattttttgg 240

OY 241 tgcattatacaaacaccacttaagtactatcataatctcttactcgtgtcctt 300
|||||
DB 241 tgcattatacaaacaccacttaagtactatcataatctcttactcgtgtcctt 300
OY 301 tgaattctgaaaaaaagctgaaaggcagaagcaagccttccacatgagcgcc 360
|||||
DB 301 tgaattctgaaaaaaagctgaaaggcagaagcaagccttccacatgagcgcc 360
OY 361 ccaatctgtcttctcgtcctatgtaactacggaactctgattctcaatgtagtgccttcgc 420
|||||
DB 361 ccaatctgtcttctcgtcctatgtaactacggaactctgattctcaatgtagtgccttcgc 420
OY 421 atcgtgcttagctgaagacc 440
|||||
DB 421 atcgtgcttagctgaagacc 440

RESULT 4

AAH83992
ID AAH83992 standard; DNA: 487 BP.

AC AAH83992;

DT 25-SEP-2001 (first entry)

DE Hylobates lar olfactory receptor encoding gene 4.

XX Olfactory receptor; primate; mouse; human; food processing industry;

KW aromas; perfumery; toxic substance; ds.

XX Hylobates lar.

PN WO200146262-A2.

PD 28-JUN-2001.

PF 22-DEC-2000; 2000WO-IB02017.

PR 22-DEC-1999; 99US-0171746.

PR 21-DEC-2000; 2000US-0747155.

XX (CNRS) CNRS CENT NAT RECH SCI.

PI Rouquier S, Giorgi D;

XX WPI; 2001-381911/40.

DR P-PSDB; AAG98506.

XX Nucleic acids encoding primate and murine olfactory receptors, useful

PT for analysis odours e.g. in food processing and perfumery -

PS Claim 1; Page 238; 482pp; English.

XX The invention relates to olfactory receptors (AAG98432-AA98609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours).

XX Sequence 487 BP; 129 A; 107 C; 78 G; 173 T; 0 other;

Query Match 38.0%; Score 185; DB 22; Length 487;

Best Local Similarity 98.9%; Pred. No. 1.2e-82;

Matches 435; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 tgaagcacaatgtaacccctgtcttaccagtgatgagtgacaaacaactcagcgctca 60

DB 1 tgaagcacaatgtaacccctgtcttaccagtgatgagtgacaaacaactcagcgctca 60

OY 61 gtgctgaagtattcatatgtaattggttccctgcacccctcgtgtcattgagatttact 120

```
Db      61 |gtgtcgaagcattcatatgtaattggtttccgcacatccctcgttcaatgtgagttact 120
Oy      121 |attgcacacacttctgcaggtttacataataattatttactgtgaatttaca 180
Db      121 |attgcacacacttctgcaggtttacataataattatttactgtgaaatttaca 180
Oy      181 |actgttcaaaatttcataatgtaatggtccatctattaaagcacaataataatttttg 240
Db      181 |actgttcaaaatttcataatgtaatggtccatctattaaagcacaataataatttttg 240
Oy      241 |tgctttatatacaataatcccaatttaagtactatcataaattcttactgtgtctctt 300
Db      241 |tgctttatatacaataatcccaatttaagtactatcataaattcttactgtgtctctt 300
Oy      301 |tgaattctgaaaaaaagtcgaaaaggcagaagcaaaagccttccacatgcagcgcc 360
Db      301 |tgaattctgaaaaaaagtcgaaaaggcagaagcaaaagccttccacatgcagcgcc 360
Oy      361 |ccatctgcttctctgtctcatgtgtactacggaactctgattctcatgtatgtgcctgc 420
Db      361 |ccatctgcttctctgtctcatgtgtactacggaactctgattctcatgtatgtgcctgc 420
Oy      421 |atctgctttagctgaaagacc 440
Db      421 |atctgctttagctgaaagacc 440
```

```
RESULT 5
AAH32168
ID      AAH32168 standard; DNA; 988 BP.
XX
XX      AAH32168;
AC
XX      30-JUL-2001 (first entry)
DT
XX      Human olfactory receptor polynucleotide, SEQ ID NO: 741.
DE
XX      Human; olfactory receptor; OR; primary scent determination;
KW      secondary scent determination; polypeptide library; odour receptor;
KW      scent profile; scent fingerprint; scent representation; ds.
XX
XX      Homo sapiens.
OS
XX      WO200127156-A2.
PN
XX      19-APR-2001.
PD
XX      06-OCT-2000; 2000WO-US27582.
PF
XX      08-OCT-1999; 990US-0158615.
PR      24-FEB-2000; 2000US-0184809.
XX
XX      (DIGI-) DIGISCENTS.
PA      (YEDA ) YEDA RES & DEV CO LTD.
XX
XX      Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
PI      WPI: 2001-290713/30.
DR
XX      New polynucleotides which encode polypeptides involved in olfactory
XX      sensation for identifying olfactory agonists and antagonists -
XX
XX      Claim 8; Page 478; 1857pp; English.
PS
XX      The present sequence is one of a number of isolated polynucleotides
CC      which encode polypeptides involved in olfactory sensation. The
CC      polynucleotides can be used in screening for olfactory agonists and
CC      antagonists. The methods allow for the determination of primary
CC      scents and the identification of the odour receptors used to detect
CC      these primary scents. The methods also enable determination of
CC      secondary scents and the identification of combinations of odour
CC      receptors that are involved in detecting such secondary scents.
```

```
CC      This enables the construction of a scent representation (also called
CC      a scent fingerprint or scent profile), which may be used to re-create
CC      and edit scents. Libraries of olfactory receptors are useful for
CC      determining the interaction pattern of a composition with the receptors,
CC      and can be used for determining differences in the olfactory facilities
CC      of different individuals.
XX
XX      Sequence 988 BP; 250 A; 231 C; 165 G; 342 T; 0 other;
SQ
XX
Query Match          6.0%; Score 29; DB 22; Length 988;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      152 |atcattattctcactgtgaatttaca 180
Db      521 |atcattattctcactgtgaatttaca 549
RESULT 6
AAI99556
ID      AAI99556 standard; cDNA; 953 BP.
XX
XX      AAI99556;
AC
XX      04-JAN-2002 (first entry)
DT
XX      Human expressed polynucleotide SEQ ID NO 19.
DE
XX
XX      Human; nootropic; neuroprotective; cytosolic; dermatological; virocidic;
KW      immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW      antiparkinsonian; anticlokling; antianaemic; antiarthritic; cancer;
KW      antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW      antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW      antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW      neurological disease; infection; nephrotropic; gene therapy; vaccine;
KW      ss.
XX
XX      Homo sapiens.
OS
XX      WO200155387-A1.
PN
XX      02-AUG-2001.
PD
XX      17-JAN-2001; 2001WO-US01310.
PF
XX      31-JAN-2000; 2000US-0179065.
PR      04-FEB-2000; 2000US-0180628.
XX      24-FEB-2000; 2000US-0184664.
PR      02-MAR-2000; 2000US-0186350.
PR      16-MAR-2000; 2000US-0189874.
PR      17-MAR-2000; 2000US-0190076.
PR      18-APR-2000; 2000US-0198123.
PR      19-MAY-2000; 2000US-0205515.
PR      07-JUN-2000; 2000US-0209467.
PR      28-JUN-2000; 2000US-0214886.
PR      30-JUN-2000; 2000US-0215135.
PR      07-JUL-2000; 2000US-0216647.
PR      11-JUL-2000; 2000US-0217487.
PR      11-JUL-2000; 2000US-0217496.
PR      14-JUL-2000; 2000US-0218290.
PR      26-JUL-2000; 2000US-0220964.
PR      26-JUL-2000; 2000US-0220963.
PR      14-AUG-2000; 2000US-0224518.
PR      14-AUG-2000; 2000US-0224519.
PR      14-AUG-2000; 2000US-0225213.
PR      14-AUG-2000; 2000US-0225214.
PR      14-AUG-2000; 2000US-0225266.
PR      14-AUG-2000; 2000US-0225267.
PR      14-AUG-2000; 2000US-0225268.
PR      14-AUG-2000; 2000US-0225270.
PR      14-AUG-2000; 2000US-0225447.
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PR 14-AUG-2000: 2000US-0225757.
PR 14-AUG-2000: 2000US-0225758.
PR 14-AUG-2000: 2000US-0225759.
PR 18-AUG-2000: 2000US-0226279.
PR 22-AUG-2000: 2000US-0226681.
PR 22-AUG-2000: 2000US-0226688.
PR 22-AUG-2000: 2000US-0227182.
PR 23-AUG-2000: 2000US-0227009.
PR 30-AUG-2000: 2000US-0228924.
PR 01-SEP-2000: 2000US-0229287.
PR 01-SEP-2000: 2000US-0229343.
PR 01-SEP-2000: 2000US-0229344.
PR 01-SEP-2000: 2000US-0229345.
PR 05-SEP-2000: 2000US-0229509.
PR 05-SEP-2000: 2000US-0229513.
PR 06-SEP-2000: 2000US-0230437.
PR 06-SEP-2000: 2000US-0230438.
PR 08-SEP-2000: 2000US-0231242.
PR 08-SEP-2000: 2000US-0231243.
PR 08-SEP-2000: 2000US-0231244.
PR 08-SEP-2000: 2000US-0231413.
PR 08-SEP-2000: 2000US-0231414.
PR 08-SEP-2000: 2000US-0232080.
PR 12-SEP-2000: 2000US-0232081.
PR 14-SEP-2000: 2000US-0232397.
PR 14-SEP-2000: 2000US-0232398.
PR 14-SEP-2000: 2000US-0232399.
PR 14-SEP-2000: 2000US-0232400.
PR 14-SEP-2000: 2000US-0232401.
PR 14-SEP-2000: 2000US-0233063.
PR 14-SEP-2000: 2000US-0233064.
PR 14-SEP-2000: 2000US-0233065.
PR 21-SEP-2000: 2000US-0234223.
PR 21-SEP-2000: 2000US-0234274.
PR 25-SEP-2000: 2000US-0234997.
PR 25-SEP-2000: 2000US-0234998.
PR 26-SEP-2000: 2000US-0235484.
PR 27-SEP-2000: 2000US-0235834.
PR 27-SEP-2000: 2000US-0235836.
PR 29-SEP-2000: 2000US-0236327.
PR 29-SEP-2000: 2000US-0236367.
PR 29-SEP-2000: 2000US-0236368.
PR 29-SEP-2000: 2000US-0236369.
PR 29-SEP-2000: 2000US-0236370.
PR 02-OCT-2000: 2000US-0236802.
PR 02-OCT-2000: 2000US-0237037.
PR 02-OCT-2000: 2000US-0237038.
PR 02-OCT-2000: 2000US-0237039.
PR 13-OCT-2000: 2000US-0237040.
PR 13-OCT-2000: 2000US-0239935.
PR 13-OCT-2000: 2000US-0239937.
PR 20-OCT-2000: 2000US-0240960.
PR 20-OCT-2000: 2000US-0241221.
PR 20-OCT-2000: 2000US-0241785.
PR 20-OCT-2000: 2000US-0241786.
PR 20-OCT-2000: 2000US-0241787.
PR 20-OCT-2000: 2000US-0241808.
PR 20-OCT-2000: 2000US-0241809.
PR 20-OCT-2000: 2000US-0241826.
PR 01-NOV-2000: 2000US-0244617.
PR 08-NOV-2000: 2000US-0246474.
PR 08-NOV-2000: 2000US-0246475.
PR 08-NOV-2000: 2000US-0246476.
PR 08-NOV-2000: 2000US-0246477.
PR 08-NOV-2000: 2000US-0246478.
PR 08-NOV-2000: 2000US-0246523.
PR 08-NOV-2000: 2000US-0246524.
PR 08-NOV-2000: 2000US-0246525.
PR 08-NOV-2000: 2000US-0246526.
PR 08-NOV-2000: 2000US-0246527.
PR 08-NOV-2000: 2000US-0246528.
PR 08-NOV-2000: 2000US-0246532.

PR 08-NOV-2000: 2000US-0246609.
PR 08-NOV-2000: 2000US-0246610.
PR 08-NOV-2000: 2000US-0246611.
PR 08-NOV-2000: 2000US-0246613.
PR 17-NOV-2000: 2000US-0249207.
PR 17-NOV-2000: 2000US-0249208.
PR 17-NOV-2000: 2000US-0249209.
PR 17-NOV-2000: 2000US-0249210.
PR 17-NOV-2000: 2000US-0249211.
PR 17-NOV-2000: 2000US-0249212.
PR 17-NOV-2000: 2000US-0249213.
PR 17-NOV-2000: 2000US-0249214.
PR 17-NOV-2000: 2000US-0249215.
PR 17-NOV-2000: 2000US-0249216.
PR 17-NOV-2000: 2000US-0249217.
PR 17-NOV-2000: 2000US-0249218.
PR 17-NOV-2000: 2000US-0249244.
PR 17-NOV-2000: 2000US-0249245.
PR 17-NOV-2000: 2000US-0249264.
PR 17-NOV-2000: 2000US-0249265.
PR 17-NOV-2000: 2000US-0249287.
PR 17-NOV-2000: 2000US-0249289.
PR 17-NOV-2000: 2000US-0249299.
PR 17-NOV-2000: 2000US-0249300.
PR 01-DEC-2000: 2000US-0250160.
PR 01-DEC-2000: 2000US-0250391.
PR 05-DEC-2000: 2000US-0251030.
PR 05-DEC-2000: 2000US-0251988.
PR 05-DEC-2000: 2000US-0256719.
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PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-465573/50.
P-PSDB; AAM99944.

PT Isolated digestive system associated polypeptide for treating,
PT preventing and/or prognosing disorders related to the digestive system
PT including digestive system cancers and also for testing and detection
XX e.g. diagnosis -

PS Claim 1; SEQ ID NO 19; 509pp + Sequence listing; English.
XX
XX The invention relates to novel genes (AAI99548-AAI99604) and proteins
CC (AAM99936-AAM99984) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and antagonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC Note: The sequence data for this patent did not form part of the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 953 BP; 242 A; 191 C; 181 G; 339 T; 0 other;

Query Match 4.5%; Score 22; DB 22; Length 953;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 taatacattacttctactgtga 171
|||||
DB 496 taatacattacttctactgtga 517

RESULT 7

AAH32012
ID AAH32012 standard; DNA; 915 BP.

AC AAH32012;

DT 30-JUL-2001 (first entry)

DE Human olfactory receptor polynucleotide, SEQ ID NO: 585.

XX Human; olfactory receptor; OR; primary scent determination;

KW secondary scent determination; polypeptide library; odour receptor;

KM scent profile; scent fingerprint; scent representation; ds.

XX Homo sapiens.

OS

PN WO200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

XX (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

XX New polynucleotides which encode polypeptides involved in olfactory

PT sensation for identifying olfactory agonists and antagonists -

PS Claim 8; Page 414-415; 1857pp; English.

XX The present sequence is one of a number of isolated polynucleotides

CC which encode polypeptides involved in olfactory sensation. The

CC polynucleotides can be used in screening for olfactory agonists and

CC antagonists. The methods allow for the determination of primary

CC scents and the identification of the odour receptors used to detect

CC these primary scents. The methods also enable determination of

CC secondary scents and the identification of combinations of odour

CC receptors that are involved in detecting such secondary scents.

CC This enables the construction of a scent representation (also called

CC a scent fingerprint or scent profile), which may be used to re-create

CC and edit scents. Libraries of olfactory receptors are useful for

CC determining the interaction pattern of a composition with the receptors,

CC and can be used for determining differences in the olfactory faculties

CC of different individuals.

CC

XX

SO Sequence 915 BP; 193 A; 253 C; 187 G; 282 T; 0 other;

RESULT 8
AAH32436
ID AAH32436 standard; DNA; 915 BP.

XX AAH32436;

DT 30-JUL-2001 (first entry)

DE Human olfactory receptor polynucleotide, SEQ ID NO: 1009.

XX Human; olfactory receptor; OR; primary scent determination;

KW secondary scent determination; polypeptide library; odour receptor;

KM scent profile; scent fingerprint; scent representation; ds.

XX Homo sapiens.

OS

PN WO200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

XX (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

XX New polynucleotides which encode polypeptides involved in olfactory

PT sensation for identifying olfactory agonists and antagonists -

PS Claim 8; Page 583; 1857pp; English.

XX The present sequence is one of a number of isolated polynucleotides

CC which encode polypeptides involved in olfactory sensation. The

CC polynucleotides can be used in screening for olfactory agonists and

CC antagonists. The methods allow for the determination of primary

CC scents and the identification of the odour receptors used to detect

CC these primary scents. The methods also enable determination of

CC secondary scents and the identification of combinations of odour

CC receptors that are involved in detecting such secondary scents.

CC This enables the construction of a scent representation (also called

CC a scent fingerprint or scent profile), which may be used to re-create

CC and edit scents. Libraries of olfactory receptors are useful for

CC determining the interaction pattern of a composition with the receptors,

CC and can be used for determining differences in the olfactory faculties

CC of different individuals.

CC

XX

SO Sequence 915 BP; 194 A; 252 C; 186 G; 283 T; 0 other;

Query Match 3.9%; Score 19; DB 22; Length 915;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 337 caaagccttcacatgc 355
|||||

DB 702 caaagccttcacatgc 720

RESULT 9

AAH42358
ID AAH42358 standard; CDNA; 918 BP.

XX AAH42358;

DT 18-DEC-2001 (first entry)

DE Human CDNA encoding olfactory receptor AOLFRL63.

XX Human: olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 KM ss; food additive; cosmetic; fragrance; pharmaceutical additive.
 XX
 OS Homo sapiens.
 XX
 PN WO200168805-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-US07771.
 XX
 PR 13-MAR-2000; 2000US-0188914.
 PR 24-MAR-2000; 2000US-0192033.
 PR 12-APR-2000; 2000US-0198474.
 PR 24-APR-2000; 2000US-0199335.
 PR 26-MAY-2000; 2000US-0207702.
 PR 23-JUN-2000; 2000US-0213849.
 PR 16-AUG-2000; 2000US-0226534.
 PR 07-SEP-2000; 2000US-0230732.
 PR 07-FEB-2001; 2001US-0266862.
 XX
 PA (SENO-) SENOMYX INC.
 XX
 PI Zozulya S;
 XX
 DR WPI: 2001-570867/64.
 DR P-PsDB; AA024685.
 XX
 PT Nucleic acids encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation,
 PT where the compounds can be used in the food, pharmaceutical and
 PT cosmetic industries to customise odours -
 XX
 PS Claim 1: Page 150-151; 319pp; English.
 XX
 CC The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR (a G protein-coupled receptor, GPCR), the OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence encodes a human olfactory receptor of
 CC the invention.
 CC
 SO Sequence 918 BP; 196 A; 253 C; 185 G; 284 T; 0 other;

Query Match 3.9%; Score 19; DB 22; Length 918;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 caaagcctctccacatgc 355
 ||||||||||||||||
 Db 702 caaagcctctccacatgc 720

RESULT 10
 AA004705
 ID AA004705 standard; DNA; 1037 BP.
 AC AA004705;
 XX
 DT 12-OCT-1990 (first entry)
 XX
 DE USP-Promoter-cassette USP-Pr.T7.1.
 XX
 KM Foreign DNA incorporation; recombinant DNA techniques;
 KM higher plant genome; legumin; USP-Pr.T7-1; ss.
 XX

PN DE3920034-A.
 XX
 PD 31-MAY-1990.
 XX
 PF 20-JUN-1989; 89DE-3920034.
 XX
 PR 19-SEP-1988; 88DD-0319887.
 XX
 PA (PFLA-) VE KOMB PFLANZENZUC.
 XX
 PI Bassuner R, Baumlein H, Muntz K, Hal NV, Wobus U;
 XX
 DR WPI: 1990-172459/23.
 XX
 PT Incorporation of DNA into higher plant genome - by specified
 PT recombinant DNA techniques.
 XX
 PS Disclosure; ; pp; German.
 XX
 CC The unique BglII-Ort (720-725) site is for ligating foreign DNA and the
 CC HindIII-Ort in the 3' polylinker (1032-1037) for cloning the
 CC cassette in the T1-vector pCA471. Agrobacterium tumefaciens is
 CC transfected.
 CC See also AA004703-004706.
 CC
 SO Sequence 1037 BP; 338 A; 174 C; 166 G; 359 T; 0 other;

Query Match 3.9%; Score 19; DB 11; Length 1037;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 gttttacagattataatc 478
 ||||||||||||||||
 Db 687 gttttacagattataatc 705

RESULT 11
 AA004706
 ID AA004706 standard; DNA; 1160 BP.
 AC AA004706;
 XX
 DT 12-OCT-1990 (first entry)
 XX
 DE USP-signalpeptide cassette USP-Sig.T7.
 XX
 KM Foreign DNA incorporation; recombinant DNA techniques;
 KM higher plant genome; signalpeptide; USP-Sig.T7.; ss.
 XX
 FH Key Location/Qualifiers
 FT CDS 708..877
 FT /*tag= a
 FT /product=signalpeptide
 FT 747..817
 XX
 PN DE3920034-A.
 XX
 PD 31-MAY-1990.
 XX
 PF 20-JUN-1989; 89DE-3920034.
 XX
 PR 19-SEP-1988; 88DD-0319887.
 XX
 PA (PFLA-) VE KOMB PFLANZENZUC.
 XX
 PI Bassuner R, Baumlein H, Muntz K, Hal NV, Wobus U;
 XX
 DR WPI: 1990-172459/23.
 DR P-PsDB; AAR05199.
 XX
 PT Incorporation of DNA into higher plant genome - by specified
 PT recombinant DNA techniques.

XX Disclosure; ; pp; German.
 PS
 CC The unique BglII-Ort (890-895) site is for
 CC ligating foreign DNA and the HindIII-Ort in the 3' polylinker
 CC (1155-1160) for cloning the cassette in the Ti-vector pGA471.
 CC The cassette is cloned into the binary Ti-vectors pGA471 and
 CC Agrobacterium tumefaciens is transfected.
 CC See also AA004703-Q04706.
 CC
 SO Sequence 1160 BP; 369 A; 192 C; 188 G; 411 T; 0 other;

Query Match 3.9%; Score 19; DB 11; Length 1160;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 460 gtttaccagcattataatc 478
 ||||||||||||||||||
 Db 672 gtttaccagcattataatc 690

RESULT 12

AA004704
 ID AA004704 standard; DNA; 1166 BP.

AC AA004704;

DT 12-OCT-1990 (first entry)

DE USP-Promoter-cassette USP-Pr.T7.2.

XX Foreign DNA incorporation; recombinant DNA techniques;
 KW higher plant genome; legumin; USP-Pr.T7-2; ss.

PN DE3920034-A.

PD 31-MAY-1990.

PF 20-JUN-1989; 89DE-3920034.

PR 19-SEP-1988; 88DD-0319887.

PA (PFLA-) VE KOMB PFLANZENZUC.

PI Bassuner R, Baumlain H, Muntz K, Hal NV, Wobus U;

DR WPI, 1990-172459/23.

PT Incorporation of DNA into higher plant genome - by specified
 PT recombinant DNA techniques.

PS Disclosure; ; pp; German.

CC The unique BglII-Ort (720-725) site is for ligating foreign DNA and the
 CC HindIII-Ort in the 3' polylinker (1261-1266) for cloning the
 CC cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
 CC transfected.
 CC See also AA004703-Q04706.
 CC
 SO Sequence 1166 BP; 381 A; 208 C; 196 G; 381 T; 0 other;

Query Match 3.9%; Score 19; DB 11; Length 1166;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 460 gtttaccagcattataatc 478
 ||||||||||||||||||
 Db 687 gtttaccagcattataatc 705

RESULT 13

ABL14992/C
 ID ABL14992 standard; cDNA; 4809 BP.

AC ABL14992;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39458.

KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.

XX Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR P-PSDB; ABB70889.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS Claim 1; SEQ ID NO 39458; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 4809 BP; 1309 A; 909 C; 1025 G; 1566 T; 0 other;

Query Match 3.9%; Score 19; DB 23; Length 4809;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 219 cactaataattattttt 237
 ||||||||||||||||||
 Db 470 CACTAATAATTATTATTTT 452

RESULT 14

AA24554
 ID AA24554 standard; cDNA; 494 BP.

AC AA24554;

DT 07-DEC-1999 (first entry)

DE Human lung tumor associated polynucleotide.

KW Human; lung tumor; lung cancer; T cell stimulation; ss.

OS Homo sapiens.

XX MO9947674-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 17-MAR-1999; 99WO-0505798.
 XX
 PR 18-MAR-1998; 98US-0040802.
 PR 18-MAR-1998; 98US-0040984.
 PR 27-JUL-1998; 98US-0123912.
 PR 27-JUL-1998; 98US-0123933.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Reed SG, Wang T;
 XX
 DR WPI; 1999-571839/48.
 XX
 PT New isolated lung tumor polynucleotides, used to develop products for
 PT the treatment, prevention and monitoring the progression of lung cancer
 PT
 PS Claim 1: Page 81; 148pp; English.
 XX
 CC The invention provides isolated human lung tumor nucleic acids and
 CC polypeptides. The polypeptides can be used for the treatment of lung
 CC cancer. The polypeptides and polynucleotides can be used to stimulate T
 CC cells or antigen presenting cells for use in the treatment of lung
 CC cancer. The polypeptides and monoclonal antibodies specific for the
 CC polypeptides can also be used to inhibit the development of lung cancer.
 CC Agents which bind the polypeptides can be used for detecting lung cancer
 CC and for monitoring the progression of lung cancer.
 XX
 SQ Sequence 494 BP; 164 A; 75 C; 81 G; 171 T; 3 other;

Query Match 3.7%; Score 18; DB 20; Length 494;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 tgaagaaggcagaagcaa 339
 ||||||||||||||||
 Db 166 tgaagaaggcagaagcaa 183

RESULT 15
 AAC65793
 ID AAC65793 standard; cDNA; 494 BP.
 XX
 AC AAC65793;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE Human lung cancer-associated cDNA LST-S1-H2-1G.
 XX
 KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection; ss.
 OS Homo sapiens.
 OS
 PN WO200061612-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 03-APR-2000; 2000WO-US08896.
 XX
 PR 02-APR-1999; 99US-0285479.
 PR 17-DEC-1999; 99US-0466396.
 PR 30-DEC-1999; 99US-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX
 PA (CORI-) CORIXA CORP.

XX
 PI Wang T, Fan L;
 XX
 DR WPI; 2000-628399/60.
 XX
 PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient -
 PS Claim 1a; Page 114; 261pp; English.
 XX
 CC This invention describes a novel isolated polypeptide (P1) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 XX
 SQ Sequence 494 BP; 164 A; 75 C; 81 G; 171 T; 3 other;

Query Match 3.7%; Score 18; DB 21; Length 494;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 322 tgaagaaggcagaagcaa 339
 ||||||||||||||||
 Db 166 tgaagaaggcagaagcaa 183

Search completed: June 27, 2002, 13:12:29
 Job time: 3942 sec

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OM nucleic - nucleic search, using sw model

Run on: June 27, 2002, 11:20:57 ; Search time 43.38 Seconds
(without alignments) 2757.573 Million cell updates/sec

Title: US-09-747-155-224

Perfect score: 487
Sequence: 1 tggatcattatgtatccct.....cgattataatccctgcta 487

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued_patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	3.7	494	US-09-040-984-54	Sequence 54, Appl
2	18	3.7	494	US-09-123-912-54	Sequence 54, Appl
3	17	3.5	4247	US-08-061-465-2	Sequence 2, Appl
4	17	3.5	6828	US-08-061-465-1	Sequence 1, Appl
5	16	3.3	546	US-08-971-090-1	Sequence 1, Appl
6	16	3.3	546	US-09-046-479-3	Sequence 3, Appl
7	16	3.3	600	PCT-US93-10418-1	Sequence 1, Appl
8	16	3.3	1128	US-08-448-744-6	Sequence 6, Appl
9	16	3.3	1992	US-08-776-265-6	Sequence 6, Appl
10	16	3.3	2481	US-08-467-568-1	Sequence 1, Appl
11	16	3.3	2481	US-09-030-582-1	Sequence 1, Appl
12	16	3.3	2481	PCT-US94-09051-1	Sequence 1, Appl
13	16	3.3	3100	US-08-296-362-1	Sequence 1, Appl
14	16	3.3	4565	US-08-776-265-1	Sequence 1, Appl
15	16	3.3	5024	US-08-920-812-7	Sequence 7, Appl
16	16	3.3	5024	US-08-920-812-7	Sequence 7, Appl
17	16	3.3	5024	US-08-920-812-7	Sequence 7, Appl
18	16	3.3	5024	US-08-921-177-7	Sequence 7, Appl
19	16	3.3	5024	US-08-362-577C-7	Sequence 7, Appl
20	16	3.3	5024	US-08-920-828-7	Sequence 7, Appl
21	15	3.1	471	US-08-222-177A-29	Sequence 29, Appl
22	15	3.1	471	US-08-502-535B-1	Sequence 1, Appl
23	15	3.1	471	US-08-908-005A-1	Sequence 1, Appl
24	15	3.1	471	US-08-558-818-6	Sequence 6, Appl
25	15	3.1	471	US-08-974-469A-6	Sequence 6, Appl
26	15	3.1	471	US-08-832-180-3	Sequence 3, Appl
27	15	3.1	471	US-08-832-198-10	Sequence 10, Appl
				US-09-253-523-1	Sequence 1, Appl

28	15	3.1	471	US-09-251-911-1	Sequence 1, Appl
29	15	3.1	510	US-08-820-170A-23	Sequence 23, Appl
30	15	3.1	510	US-09-055-699-23	Sequence 23, Appl
31	15	3.1	510	US-09-273-565-23	Sequence 23, Appl
32	15	3.1	510	US-09-565-538-23	Sequence 23, Appl
33	15	3.1	617	US-08-820-170A-24	Sequence 24, Appl
34	15	3.1	617	US-09-055-699-24	Sequence 24, Appl
35	15	3.1	617	US-09-273-565-24	Sequence 24, Appl
36	15	3.1	617	US-09-565-538-24	Sequence 24, Appl
37	15	3.1	662	US-08-998-416-185	Sequence 185, App
38	15	3.1	662	US-08-998-416-191	Sequence 191, App
39	15	3.1	665	US-08-998-416-937	Sequence 937, App
40	15	3.1	669	US-08-896-410-3	Sequence 3, Appl
41	15	3.1	701	US-08-998-416-701	Sequence 701, App
42	15	3.1	711	US-08-998-416-786	Sequence 786, App
43	15	3.1	724	US-08-998-416-683	Sequence 683, App
44	15	3.1	732	US-08-998-416-1036	Sequence 1036, Ap
45	15	3.1	767	US-08-998-416-472	Sequence 472, App

ALIGNMENTS

RESULT 1
US-09-040-984-54
Sequence 54, Application US/09040984
Patent No. 6210883
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF LUNG CANCER
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040.984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-282-6031
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-040-984-54

Query Match 3.7%; Score 18; DB 4; Length 494;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 tgaagaagcagaagca 339
|||||
Db 166 TGAAGAAGCGAAGCA 183

RESULT 2
US-09-123-912-54
Sequence 54, Application US/09123912A
Patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tonglong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 494
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (431)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (442)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (445)
OTHER INFORMATION: where n is a, c, g or t
US-09-123-912-54

Query Match 3.7%: Score 18; DB 4; Length 494;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 tgaagaagcagaagca 339
|||||
DB 166 tgaagaagcagaagca 183

RESULT 3
US-08-061-465-2/C
Sequence 2, Application US/08061465
Patent No. 5625049
GENERAL INFORMATION:
APPLICANT: Monroe, Stephan S.
APPLICANT: Glass, Roger I.
APPLICANT: Koopmans, Marion
APPLICANT: Jiang, Baoming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING HUMAN ASTROVIRUS
TITLE OF INVENTION: SEROTYPE II AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: 127 Peachtree Street, N.E.
STREET: Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,465
FILING DATE: 19930512
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.

REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4247 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human Astrovirus
STRAIN: Serotype 2
US-08-061-465-2

Query Match 3.5%: Score 17; DB 1; Length 4247;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 gatattctgaaaaaaa 318
|||||
DB 3021 GATATTCTGAAAAAAA 3005

RESULT 4
US-08-061-465-1/C
Sequence 1, Application US/08061465
Patent No. 5625049
GENERAL INFORMATION:
APPLICANT: Monroe, Stephan S.
APPLICANT: Glass, Roger I.
APPLICANT: Koopmans, Marion
APPLICANT: Jiang, Baoming
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING HUMAN ASTROVIRUS
TITLE OF INVENTION: SEROTYPE II AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: 127 Peachtree Street, N.E.
STREET: Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,465
FILING DATE: 19930512
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6828 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Human Astrovirus
STRAIN: Serotype 2
POSITION IN GENOME:
UNITS: 1008
US-08-061-465-1

Query Match 3.5%; Score 17; DB 1; Length 6828;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 gatatctgaaaaaaa 318
|||||
Db 3103 GATATCTGAAAAAAA 3087

RESULT 5
US-08-971-090-1/c
Sequence 1, Application US/08971090
Patent No. 6228579
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith W.
APPLICANT: Forsyth, R. Allyn
TITLE OF INVENTION: METHOD FOR IDENTIFYING MICROBIAL PROLIFERATION GENES
FILE REFERENCE: 07252/008001
CURRENT APPLICATION NUMBER: US/08/971.090
CURRENT FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 546
TYPE: RNA
ORGANISM: E. coli
US-08-971-090-1

Query Match 3.3%; Score 16; DB 4; Length 546;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ttgcttatccagtg 35
|||||
Db 268 TTCCTTATCCAGTGA 253

RESULT 6
US-09-046-479-3/c
Sequence 3, Application US/09046479
Patent No. 6291653
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Delsher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046.479
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 40...396
OTHER INFORMATION:
US-09-046-479-3

Query Match 3.3%; Score 16; DB 4; Length 546;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 ttctcgatccctcg 103
|||||
Db 160 TTCCTGCATCCTCTG 145

RESULT 7
PCT-US93-10418-1
Sequence 1, Application PC/TUS9310418
GENERAL INFORMATION:
APPLICANT: Ziegler, Steven F.
APPLICANT: Hjerrild, Kathryn A.
TITLE OF INVENTION: Activation Antigen CD69
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10418
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2610-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 1..600
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 1..597
PCT-US93-10418-1

Query Match 3.3%; Score 16; DB 5; Length 600;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 ttattctactgtgaa 172
|||||
DB 293 TTATTCTACTGTGAA 308

RESULT 8
US-08-448-744-6/c
Sequence 6, Application US/08448744
Patent No. 5616484
GENERAL INFORMATION:
APPLICANT: XU, Shuang-yong
TITLE OF INVENTION: Cloning And Expression of The Apali
TITLE OF INVENTION: Restriction Endonuclease
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: New England Biolabs, Inc.
STREET: 32 Tozer Road
CITY: Beverly
STATE: Massachusetts
COUNTRY: US
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,744
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-448-744-6

Query Match 3.3%; Score 16; DB 1; Length 1128;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 aactcgtatctcatg 406
|||||
DB 1096 AACTCTGATCTCATG 1081

RESULT 9
US-08-776-265-6/c
Sequence 6, Application US/08776265
Patent No. 6001631
GENERAL INFORMATION:

APPLICANT: BLANCHE, Francis
APPLICANT: CAMERON, Beatrice
APPLICANT: CROUZET, Joel
APPLICANT: FAMECHON, Alain
APPLICANT: FERRERO, Lucia
TITLE OF INVENTION: No. 6001631el Topoisomerase IV, Corresponding
TITLE OF INVENTION: Nucleotide Sequences and Uses Thereof
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I. Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,265
FILING DATE: 24-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32, 220
REFERENCE/DOCKET NUMBER: 03806.0394-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4444
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-776-265-6

Query Match 3.3%; Score 16; DB 3; Length 1992;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 ttacagattataatt 478
|||||
DB 1495 TTACAGATTATTAATT 1480

RESULT 10
US-08-467-568-1/c
Sequence 1, Application US/08467568
Patent No. 5817477
GENERAL INFORMATION:
APPLICANT: SOPPET, DANIEL R
TITLE OF INVENTION: ADRENERGIC RECEPTOR
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gillilan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,568
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 101..1687
US-08-467-568-1

Query Match 3.3%; Score 16; DB 1; Length 2481;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 aataatattttttt 238
|||||

Db 2467 AATAATATTATTTT 2452

RESULT 11
US-09-030-582-1/c
Sequence 1, Application US/09030582
Patent No. 5994506
GENERAL INFORMATION:
APPLICANT: SOPPET, DANIEL R
TITLE OF INVENTION: ADRENERGIC RECEPTOR
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,582
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 101..1687
US-09-030-582-1

Query Match 3.3%; Score 16; DB 2; Length 2481;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 aataatattttttt 238
|||||

Db 2467 AATAATATTATTTT 2452

RESULT 12
PCT-US94-09051-1/c
Sequence 1, Application PC/TUS9409051
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Adrenergic Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CECCHI, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09051
FILING DATE: Submitted herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US94-09051-1

Query Match 3.3%; Score 16; DB 5; Length 2481;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 aataatattttttt 238
|||||

Db 2467 AATAATATTATTTT 2452

RESULT 13
US-08-296-362-1/c
Sequence 1, Application US/08296362
Patent No. 5691306

GENERAL INFORMATION:
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
APPLICANT: Mado, Ikuro
TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
TITLE OF INVENTION: PROTEIN TRAFICKING DISORDERS AND INCREASING SECRETORY
TITLE OF INVENTION: PROTEIN PRODUCTION
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,362
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deehr, Manya S.
REGISTRATION NUMBER: 37,120
REFERENCE/DOCKET NUMBER: 690066.401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 102..1883
US-08-296-362-1

Query Match 3.3%; Score 16; DB 1; Length 3100;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 182 cgtctcaaatcatt 197
|||||
Db 1849 CTTCTCAAAATTTCAT 1834

RESULT 14
US-08-776-265-1/c
Sequence 1, Application US/08776265
Patent No. 6001631
GENERAL INFORMATION:
APPLICANT: BLANCHE, Francis
APPLICANT: CAMERON, Beatrice
APPLICANT: CROUZET, Joel
APPLICANT: FAMECHON, Alain
APPLICANT: FERRERO, Lucia
TITLE OF INVENTION: No. 6001631el Topoisomerase IV, Corresponding
TITLE OF INVENTION: Nucleotide Sequences and Uses Thereof
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flunegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I. Street, N.W., Suite 700
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,265
FILING DATE: 24-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 03806.0394-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4444
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-776-265-1

Query Match 3.3%; Score 16; DB 3; Length 4565;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 463 ttacacgattataatt 478
|||||
Db 1535 TTACACGATTATAATT 1520

RESULT 15
US-08-920-812-7/c
Sequence 7, Application US/08920812
Patent No. 5763188
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5024 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus epidermidis
STRAIN: Clinical Isolate SE-32
US-08-920-812-7

Query Match 3.38; Score 16; DB 1; Length 5024;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 aattggttctcat 97
|||||
Db 1574 AATTGTTCTCAT 1559

Search completed: June 27, 2002, 13:08:46
Job time: 6469 sec

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